PCT/AU2004/000493

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Patents Act 1990

PROVISIONAL SPECIFICATION

Invention Title: **Manipulation of organic acid biosynthesis and secretion**

The invention is described in the following statement:

MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid metabolism (CAM) photosynthesis, stomatal and pulvinual movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation Al^{3+} which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors NAD^+ and FAD, forming NADH, $FADH_2$, and carbon dioxide (CO_2). The reaction sequence of the TCA cycle involves: in a reaction catalyzed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C_6 tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of CO_2 in a series of reactions that leads to the formation of one oxaloacetate, three NADH, one $FADH_2$, and one ATP. The resulting oxaloacetate reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional CO_2 and NADH. Thus the TCA cycle brings about the complete oxidation of pyruvate to three CO_2 plus 10 electrons, which are stored temporarily as 4 NADH and 1 $FADH_2$.

Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form CO_2, acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well as free coenzyme A (CoASH) and NAD^+, links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate carboxylase.

In particular, citrate synthase (CS) catalyzes the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyzes the final step of the TCA cycle, oxidizing malate to oxaloacetate and producing NADH. This reaction catalyzed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an $NADP^+$-dependent MDH that plays a critical role in balancing reducing equivalents between the cytosol and stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in β-oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and

alfalfa (*Medicago sativa*), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of N_2 by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyzes the reaction of phosphoenol-pyruvate with HCO_3^- releasing the phosphate and producing the C4 product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malata dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO_2 fixation in C_4 and Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorous acquisition efficiency in plants; in modifying aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic enzymes CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species which are related to CS, MDH and PEPC, or functionally active fragments or variants thereof. Such proteins are referred to herein as CS-like, MDH-like and PEPC-like respectively.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene

activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses,

respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

The term "purified" means that the nucleic acid or polypeptide is substantially free of other nucleic acids or polypeptides.

By "functionally active" in respect of a nucleotide sequence it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

By "functionally active" in the context of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence.. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

By "operatively linked" in respect of a regulatory element, nucleic acid or nucleic acid fragment and terminator, it meant that the regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an CS or CS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (b) complements of the sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MDH or MDH-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (b) complements of the sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an PEPC or PEPC-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86,

88, 89, 91, 92, 94, 95 and 97 hereto; (b) complements of the sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman *et al.* (1988) *Proc. Natl. Acad Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or

5' cDNA fragments may be isolated (Ohara *et al.* (1989) *Proc. Natl. Acad Sci USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 10, 185 and 188 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96 and 98 hereto, and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 79, 89, 92, 104, 122, 131, 142, 145, 148, 151, 154, 157, 163, 173, 179, 186, 189, 192, 200, 203, 209, 226, 232, 246, 255 and 262 hereto.

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 66, 67, 72, 78, 88, 94, 101and 104 hereto; or complements or sequences antisense thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence

information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic acid soils; in relation to nutrient acquisition efficiency including phosphorus; in relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the

desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue specific promoters include root prevalent promoters.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*) and the octopine synthase (*ocs*) genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such

techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying organic acid biosynthesis; of modifying organic acid secretion; of modifying phosphorous and other nutrients acquisition efficiency in plants; of modifying aluminium and acid soil tolerance in plants; of modifying nitrogen fixation and nodule function, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to the present invention. Preferably the nucleic acid or nucleic acid fragment is part of a vector.

Using the methods and products of the present invention, organic acid biosynthesis; organic acid secretion; phosphorous and other plant nutrient acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and nodule function, may be increased or otherwise altered, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise altered, for example

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by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSd.

Figure 10 shows the deduced amino acid sequence of LpCSd.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb.

Figure 15 shows the deduced amino acid sequence of LpMDHb.

Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc.

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

Figure 21 shows the nucleotide sequence of LpMDHe.

Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

Figure 26 shows the nucleotide sequence of LpMDHg.

Figure 27 shows the deduced amino acid sequence of LpMDHg.

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

Figure 31 shows the nucleotide sequence of LpMDHi.

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHl.

Figure 39 shows the deduced amino acid sequence of LpMDHl.

Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

Figure 62 shows the deduced amino acid sequence of TrMDHc.

Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj.

Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa.

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

Figure 93 shows the deduced amino acid sequence of TrPEPCc.

Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc.

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

Figure 97 shows the nucleotide sequence of TrPEPCe.

Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1

cDNA libraries from white clover (Trifolium repens)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 &28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated wc
04wc	Nodulated wc cut leaf and stem collected after 0, 1, 4, 6 &14 h after cutting
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials

Library	Organ/Tissue
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2

cDNA libraries from perennial ryegrass (Lolium perenne)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development

Library	Organ/Tissue
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (*rbcL, rbcS, cab, wir2A* subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2

DNA sequence analyses

The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to

a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

Agriculture Victoria Services Pty Ltd

and

AgResearch Limited

By their Registered Patent Attorneys

Freehills Carter Smith Beadle **14 April 2003**

Figure 1 Consensus contig nucleotide sequence of LpCSa

```
                 *       20         *       40         *       60
LpCSa : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT :  60

                 *       80         *      100         *      120
LpCSa : GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC : 120

                 *      140         *      160         *      180
LpCSa : CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG : 180

                 *      200         *      220         *      240
LpCSa : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 240

                 *      260         *      280         *      300
LpCSa : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300

                 *      320         *      340         *      360
LpCSa : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 360

                 *      380         *      400         *      420
LpCSa : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCTTCAAA : 420

                 *      440         *      460         *      480
LpCSa : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 480

                 *      500         *      520         *      540
LpCSa : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 540

                 *      560         *      580         *      600
LpCSa : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 600

                 *      620         *      640         *      660
LpCSa : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 660

                 *      680         *      700         *      720
LpCSa : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 720

                 *      740         *      760         *      780
LpCSa : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA : 780

                 *      800         *      820         *      840
LpCSa : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG : 840

                 *      860         *      880         *      900
LpCSa : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT : 900

                 *      920         *      940         *      960
LpCSa : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 960
```

```
                  *       980         *       1000        *       1020
LpCSa : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 1020

                  *      1040         *       1060        *       1080
LpCSa : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 1080

                  *      1100         *       1120        *       1140
LpCSa : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 1140

                  *      1160         *       1180        *       1200
LpCSa : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 1200

                  *      1220         *       1240        *       1260
LpCSa : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 1260

                  *      1280         *       1300        *       1320
LpCSa : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 1320

                  *      1340         *       1360        *       1380
LpCSa : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 1380

                  *      1400         *       1420        *       1440
LpCSa : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 1440

                  *      1460         *       1480        *       1500
LpCSa : TATCTTGAAAGTCTTAATCATGTGGACCAATGAAGACATAGATCAAGTTCTTTGCATGGG : 1500

                  *      1520         *       1540        *
LpCSa : CGGCGGCTGTTTCTTTGGGAAAAAACTTTTTATGGAGTCTTTTTTTACC : 1550
```

Figure 2 Deduced amino acid sequence of LpCSa

```
                   *        20         *        40         *        60
LpCSa : YIDGDEGILRYRGYPIEEVAESSSFVEVAYLLMYGNLPTQSQLAGWEFAISQHSAVPQGL :  60

                   *        80         *       100         *       120
LpCSa : LDIIQSMPHDAHPMGVLASAMSTLSVFHPDANPALRGQDLYKSKQVRDKQIVRVLGKAPV : 120

                   *       140         *       160         *       180
LpCSa : IAAAAYLRLAGRPFVLPSNNLSYSENFLYMLDSMGDKDYKPNPRLARVLDVLFILHAEHE : 180

                   *       200         *       220         *       240
LpCSa : MNCSTAAVRHLASSGVDVFTALSGAVGALYGPLHGGANEAVLKMLNEIGSVENIPEFIEG : 240

                   *       260         *       280         *       300
LpCSa : VKNRKRKMSGFGHRVYKNYDPRAKVIRKLAEEVFTIVGRDPLIEVAVALEKAALSDEYFI : 300

                   *       320         *       340         *       360
LpCSa : KRKLYPNVDFYSGLIYRAMGFPTEFFPVLFAVPRMAGWLAHWKESLDDPDNKIMRPQQVY : 360

                   *       380         *       400
LpCSa : TGTWLRHYTPVRERVPSSDSEQLGQIATSNATRRRRAGSAL : 401
```

Figure 3 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSa

```
                       *        20         *        40         *        60
LpCSa1 : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT :  60
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                       *        80         *       100         *       120
LpCSa1 : GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC : 120
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                       *       140         *       160         *       180
LpCSa1 : CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG : 180
LpCSa2 : --------------GCAGGCTGGGAGTTTGCAATTTCGCA-CACTCTGCTGTTCCTCANGN :  46
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                       *       200         *       220         *       240
LpCSa1 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 240
LpCSa2 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 106
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                       *       260         *       280         *       300
LpCSa1 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300
LpCSa2 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 166
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -
```

```
                 *      320         *      340         *      360
LpCSa1 : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 360
LpCSa2 : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 226
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *      380         *      400         *      420
LpCSa1 : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCTTTTGTCCTTCCTTCAAA : 420
LpCSa2 : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCTTCAAA : 286
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *      440         *      460         *      480
LpCSa1 : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 480
LpCSa2 : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 346
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *      500         *      520         *      540
LpCSa1 : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 540
LpCSa2 : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 406
LpCSa3 : -----------------------------------------------NTTNTGCTG-ACA :  12
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *      560         *      580         *      600
LpCSa1 : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 600
LpCSa2 : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 466
LpCSa3 : CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT :  72
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *      620         *      640         *      660
LpCSa1 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGNGGCGCAAATGA : 660
LpCSa2 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 526
LpCSa3 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 132
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -
```

```
                   *        680         *        700         *        720
LpCSa1 : NGCGGTACTT-AAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 719
LpCSa2 : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 586
LpCSa3 : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 192
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *        740         *        760         *        780
LpCSa1 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGNTTTGGGCACN---------------- : 763
LpCSa2 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA : 646
LpCSa3 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGCTTTGGGCACCGTGTGTATAAGAATTA : 252
LpCSa4 : ----------------------------------------------------------GA :   2
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *        800         *        820         *        840
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGN------------------------ : 682
LpCSa3 : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG : 312
LpCSa4 : TTATCCTCGCGCTAAAGTCAT-CCGGAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG :  61
LpCSa5 : -----------------------GGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG :  37
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *        860         *        880         *        900
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGTAGCACTGTCAGACGAGTATTT : 372
LpCSa4 : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT : 121
LpCSa5 : GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT :  97
LpCSa6 : --------------------------------------------TNNCAGACGAGTATTT :  16
LpCSa7 : ---------------------------------------------GTCAGACGAGTATTT :  15
LpCSa8 : ------------------------------------------------------------ :   -

                   *        920         *        940         *        960
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 432
LpCSa4 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 181
LpCSa5 : TATCGAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 157
LpCSa6 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT :  76
LpCSa7 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT :  75
LpCSa8 : ------------------------------------------------------------ :   -

                   *        980         *       1000         *       1020
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 492
LpCSa4 : GGGATTCCCTGCAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 241
LpCSa5 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 217
LpCSa6 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 136
LpCSa7 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 135
LpCSa8 : ------------------------------------------------------------ :   -
```

```
                   *        1040         *        1060         *        1080
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 552
LpCSa4 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 301
LpCSa5 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 277
LpCSa6 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 196
LpCSa7 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 195
LpCSa8 : ------------------------------------------------------------ :   -

                   *        1100         *        1120         *        1140
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 612
LpCSa4 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 361
LpCSa5 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 337
LpCSa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 256
LpCSa7 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 255
LpCSa8 : ------------------------------------------------------------ :   -

                   *        1160         *        1180         *        1200
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : CAGTGAGCAGCTTGGGCAGATCACTACATCAAACGCGACGAGGCGTCGGCGTGCTGGTTC : 672
LpCSa4 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 421
LpCSa5 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 397
LpCSa6 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 316
LpCSa7 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 315
LpCSa8 : --------------GGCAGATCGCT-CATCAAACGCGTCGAGGCGTCGGCGTGCTGGCTC :  45

                   *        1220         *        1240         *        1260
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 732
LpCSa4 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 481
LpCSa5 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 457
LpCSa6 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 376
LpCSa7 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 375
LpCSa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 105

                   *        1280         *        1300         *        1320
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : AGGGCCACGGCTGCTTAAATN--------------------------------------- : 753
LpCSa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATGTAGGC : 541
LpCSa5 : AGGGCCACAGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 517
LpCSa6 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 436
LpCSa7 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 435
LpCSa8 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 165

                   *        1340         *        1360         *        1380
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 601
LpCSa5 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 577
LpCSa6 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496
LpCSa7 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 495
LpCSa8 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 225
```

```
                      *        1400         *        1420         *        1440
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 661
LpCSa5 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 637
LpCSa6 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 556
LpCSa7 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 555
LpCSa8 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 285

                      *        1460         *        1480         *        1500
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : TGTCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG : 720
LpCSa5 : TATCTTGAAAGTCTTANTCCNNNNAAAAA------------------------------- : 666
LpCSa6 : TATCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG : 615
LpCSa7 : TATCTTGAAAGTCTTAATCATGTGGACCAATCAAAAAAAAAA------------------ : 597
LpCSa8 : TATCTTGAAAGTCTTAAAAAAAAAA----------------------------------- : 310

                      *        1520         *        1540         *
LpCSa1 : -------------------------------------------------- :   -
LpCSa2 : -------------------------------------------------- :   -
LpCSa3 : -------------------------------------------------- :   -
LpCSa4 : CGGCGGCTGTTTCTTTGGNAAAAAA------------------------- : 745
LpCSa5 : -------------------------------------------------- :   -
LpCSa6 : CGGCGGCTGTTTCTTTGTGTTTCCTCTTTTTTATGGAGTCTTTTTTTACC : 665
LpCSa7 : -------------------------------------------------- :   -
LpCSa8 : -------------------------------------------------- :   -
```

Figure 4 Consensus contig nucleotide sequence of LpCSb

```
                 *        20         *        40         *        60
LpCSb : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG :  60

                 *        80         *       100         *       120
LpCSb : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120

                 *       140         *       160         *       180
LpCSb : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180

                 *       200         *       220         *       240
LpCSb : ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG : 240

                 *       260         *       280         *       300
LpCSb : CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT : 300

                 *       320         *       340         *       360
LpCSb : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360

                 *       380         *       400         *       420
LpCSb : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG : 420

                 *       440         *       460         *       480
LpCSb : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTNATGGATCAAATCTGTGATGGAAG : 480

                 *       500         *       520         *       540
LpCSb : AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA : 540

                 *       560         *       580         *       600
LpCSb : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600

                 *       620         *       640         *       660
LpCSb : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 660

                 *       680         *       700         *       720
LpCSb : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 720

                 *       740         *       760         *       780
LpCSb : GGCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 780

                 *       800         *       820         *       840
LpCSb : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 840

                 *       860         *       880         *       900
LpCSb : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG : 900

                 *       920         *       940         *       960
LpCSb : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG : 960
```

```
                    *        980         *       1000         *        1020
LpCSb : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 1020

                    *       1040         *       1060         *        1080
LpCSb : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 1080

                    *       1100         *       1120         *        1140
LpCSb : CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 1140

                    *       1160
LpCSb : GACACATAAGTTTTATGTGTCGCTCGG : 1167
```

Figure 5 Deduced amino acid sequence of LpCSb

```
                       *        20          *        40          *        60
LpCSb : SPCXCSPMTQFTTGVMALQVESEFAKAYEKGIHKSKFWEPTYEDSLNLIARLPQVASYVY :  60

                       *        80          *       100          *       120
LpCSb : RRIFKDGKTIAADNTLDYAANFSHMLGFDDPKMLELMRLYITIHTDHEGGNVSAHAGHLV : 120

                       *       140          *       160          *       180
LpCSb : GSALSDPYLSFAAALNGLAGPLHGLANQEVLXWIKSVMEETGSNITTDQLKEYVWKTLKS : 180

                       *       200          *       220          *       240
LpCSb : GKVVPGYGHGVLRNTDPRYSCQREFALKYLPEDPLFQLVSKLYEVVPPILTELGKVKNPW : 240

                       *       260          *       280          *       300
LpCSb : PNVDAHSGVLLNHFGLVEARYYTVLFGVSRSMGIGSQLIWDRALGLPLERPKSVTMEWLE : 300


LpCSb : NHCKKAAA : 308
```

ure 6 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSb

```
                  *        20         *        40         *        60
LpCSb1 : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG :  60
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *        80         *       100         *       120
LpCSb1 : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       140         *       160         *       180
LpCSb1 : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       200         *       220         *       240
LpCSb1 : ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG : 240
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       260         *       280         *       300
LpCSb1 : CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT : 300
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       320         *       340         *       360
LpCSb1 : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       380         *       400         *       420
LpCSb1 : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG : 420
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       440         *       460         *       480
LpCSb1 : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTTATGGATCAAATCTGTGATGGAAG : 480
LpCSb2 : -----------------------------------TNATGGAT-NAATCTGTGATGGAAG :  24
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                  *       500         *       520         *       540
LpCSb1 : AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA : 540
LpCSb2 : -AACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA :  83
LpCSb3 : -----------------------------------------------------CTGAAGA :   7
LpCSb4 : ------------------------------------------------------------ :   -
```

```
                  *        560         *        580         *        600
LpCSb1 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600
LpCSb2 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 143
LpCSb3 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT :  67
LpCSb4 : ------------------------------------------------------------ :   -

                  *        620         *        640         *        660
LpCSb1 : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCTGAAGACCCACTTTTCCAACTGGTCT : 660
LpCSb2 : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 203
LpCSb3 : CGTGCCAAAGGGAGTNGGNACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 127
LpCSb4 : ------------------------------------------------------------ :   -

                  *        680         *        700         *        720
LpCSb1 : CCAAGTTGTATGAAGTTGTGCCTCCTATCCTCACTGAGTTAGGCAAGGTAAAAAACCCAT : 720
LpCSb2 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 263
LpCSb3 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 187
LpCSb4 : ------------------------------------------------------------ :   -

                  *        740         *        760         *        780
LpCSb1 : GGCCTAATGTTGATGCTCACAGNGGAGTTTTGCTCAACCACTTCGGATTAGTTGAA-CAC : 779
LpCSb2 : GCCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 323
LpCSb3 : GGCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 247
LpCSb4 : ------------------------------------------------------------ :   -

                  *        800         *        820         *        840
LpCSb1 : GGNACTACACTGNCTTGNTCGGN------------------------------------- : 802
LpCSb2 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCCCATTT : 383
LpCSb3 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 307
LpCSb4 : --------------------------------------GTTTTTGGATCCCAGCTCATTT :  22

                  *        860         *        880         *        900
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG : 443
LpCSb3 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG : 367
LpCSb4 : GGGTCCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG :  82

                  *        920         *        940         *        960
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG : 503
LpCSb3 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTNGTTTTACAAATCAN : 427
LpCSb4 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG : 142

                  *        980         *       1000         *       1020
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 563
LpCSb3 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGGTAGCCTTGTTTTACC : 487
LpCSb4 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 202

                  *       1040         *       1060         *       1080
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTTACAGACGGTAGAATTTTGTAA : 623
LpCSb3 : ATNTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 547
LpCSb4 : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 262
```

```
                  *        1100          *        1120          *        1140
LpCSb1  :  --------------------------------------------------------------------- :   -
LpCSb2  :  CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 683
LpCSb3  :  CCACCGGTACTTG-ACACCGAATNANNTAAATGGNATTTGGCATAAAGAGATTAGGACAT : 606
LpCSb4  :  CCACCGTTACTTGAACACCGAATCAGTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 322

                  *        1160
LpCSb1  :  ---------------------------- :   -
LpCSb2  :  GACACATAAGTTTTATGTGNCGNTCGG : 710
LpCSb3  :  GACACATAAGTTTTATGTGTCGCTCGG : 633
LpCSb4  :  GACACATAAGTTTTATGTGTCGCTCGA : 349
```

Figure 7 Nucleotide sequence of LpCSc

```
                     *        20         *        40         *        60
LpCSc : TCNCCGTGGCCANAATNCCCCANCATTCAAATACCGCCCGTCAGCCACCAATCCTCCTAC :  60

                     *        80         *       100         *       120
LpCSc : CTTCTTATTTCCACCCCAACCGCCCAACATGTGTCCTCCCACCGAANAAACACCTGCTAC : 120

                     *       140         *       160         *       180
LpCSc : CAACGGCCATAGCAACGGCACCAACGGCGCCAATGGCTCCAAGGAAGGCTTCACAGGCGT : 180

                     *       200         *       220         *       240
LpCSc : CACGACCAGACAGAACCCTCACCCTACACACAAGAGCCCATATGCACCTGTTGGCGACTT : 240

                     *       260         *       280         *       300
LpCSc : TTTGTCAAATGTCGGCCGCTTCAAGATTATCGAGAGCACATTAAGAGAGGGCGAGCAATT : 300

                     *       320         *       340         *       360
LpCSc : CGCCAACGCCTACTTCGACCTTGAGGCTAAAATCAAGATCGCCAGAGCTCTCGACAACTT : 360

                     *       380         *       400         *       420
LpCSc : TGGTGTTGACTACATTGAAGTTACCAGCCCTGCTGCCTCTGAGCAGTCAAGAAGGGACTG : 420

                     *       440         *       460         *       480
LpCSc : CGAAGCCCTCTGCAAGCTCGGATTGAAAGCCAAGATCCTTACCCACGTACGATGCCACAT : 480

                     *       500         *       520         *       540
LpCSc : GGACGATGCCAGAATCGCTGTCGAGACTGGTGTTGACGGCCTCGATGTCGTCATTGGAAC : 540

                     *       560         *       580         *       600
LpCSc : CTCTGCGTACCTCCGCGAGCACAGCCATGGCAAGGACATGACATACATCAAAAACACAGC : 600

                     *       620         *
LpCSc : GCTGGAGGTGATTGAGTTTGTCAAGAGCAAGGGAN : 635
```

ure 8 Deduced amino acid sequence of LpCSc

```
                   *        20          *        40          *        60
LpCSc : XRGXNXPXFKYRPSATNPPTFLFPPQPPNMCPPTEXTPATNGHSNGTNGANGSKEGFTGV :  60

                   *        80          *       100          *       120
LpCSc : TTRQNPHPTHKSPYAPVGDFLSNVGRFKIIESTLREGEQFANAYFDLEAKIKIARALDNF : 120

                   *       140          *       160          *       180
LpCSc : GVDYIEVTSPAASEQSRRDCEALCKLGLKAKILTHVRCHMDDARIAVETGVDGLDVVIGT : 180

                   *       200          *
LpCSc : SAYLREHSHGKDMTYIKNTALEVIEFVKSKG : 211
```

Figure 9   Nucleotide sequence of LpCSd

```
                 *        20         *        40         *        60
LpCSd : GTGNTATGGCNCANCCAGNANTCCTNCGTNCTGGCTNCCANANNAGNAANAAGCTATCGG :  60

                 *        80         *       100         *       120
LpCSd : CAACGACCTCAGCGATCAGGCCATCAAGGACTACCTGTGGTCCACCCTCAAGGCTGGCCA : 120

                 *       140         *       160         *       180
LpCSd : AGTCGTTCCCGGTTACGGACACGCCGTTCTCCGCAAGACCGACCCCCGCTACGTCTCCCA : 180

                 *       200         *       220         *       240
LpCSd : GCGCGAGTTCGCCCAGAAGCACCTTCCCGACGACCCAATGTTCAAGCTCGTCAGTCAGGT : 240

                 *       260         *       280         *       300
LpCSd : CTACAAGATCGCCCCTGGTGTTCTCACCGAGCACGGCAAGACCAAGAACCCCTACCCCAA : 300

                 *       320         *       340         *       360
LpCSd : CGTCGACGCCCACTCCGGTGTCCTCCTCCAGTACTACGGCCTCACTGAGCAGAACTACTA : 360

                 *       380         *       400         *       420
LpCSd : CACCGTTCTCTTCGGTGTATCCCGTGCGCTCGGTGTCCTTCCCCAGCTTATCATTGACCG : 420

                 *       440         *       460         *       480
LpCSd : TGCCGTCGGTGCCCCCATTGAGAGGCCCAAGTCTTTCAGCACTGAGGCTTACGCCAAGTT : 480

                 *       500         *       520         *       540
LpCSd : GGTTGGTGCTAAGTTGTAAGCGCGTTACTGCAACGTGCTCTACAGCCAGGAGAATGTGGA : 540

                 *       560         *       580         *       600
LpCSd : GGAATTTGTTTAACATTCAGAGATACCTTGTCCTGTGTAGAATTGCAATGTAAGGATAGG : 600

                 *       620         *
LpCSd : GAATGGGAGCGTTACGGCGCTACATCACTACATTTN : 636
```

Figure 10 Deduced amino acid sequence of LpCSd

```
                     *        20         *        40         *        60
LpCSd : XYGXXXXPXXWXPXXXXAIGNDLSDQAIKDYLWSTLKAGQVVPGYGHAVLRKTDPRYVSQ :  60

                     *        80         *       100         *       120
LpCSd : REFAQKHLPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEQNYY : 120

                     *       140         *       160
LpCSd : TVLFGVSRALGVLPQLIIDRAVGAPIERPKSFSTEAYAKLVGAKL : 165
```

Figure 11 Consensus contig nucleotide sequence of LpMDHa

```
                  *        20         *        40         *        60
LpMDHa : GGTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  60

                  *        80         *       100         *       120
LpMDHa : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGACAGAAGT : 120

                  *       140         *       160         *       180
LpMDHa : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 180

                  *       200         *       220         *       240
LpMDHa : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 240

                  *       260         *       280         *       300
LpMDHa : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 300

                  *       320         *       340         *       360
LpMDHa : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 360

                  *       380         *       400         *       420
LpMDHa : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 420

                  *       440         *       460         *       480
LpMDHa : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTTTTGACTTT : 480

                  *       500         *       520         *       540
LpMDHa : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 540

                  *       560         *       580         *       600
LpMDHa : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 600

                  *       620         *       640         *       660
LpMDHa : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAATTGGGG : 660

                  *       680         *
LpMDHa : GTGANTCCATTGGCCTCAAGCCAAAAAAAAAAAAAA : 696
```

Figure 12 Deduced amino acid sequence of LpMDHa

```
                    *        20         *        40         *        60
LpMDHa : VGCWYHHSALFSQATPSTNALSSEDIKALTKRTQEGGTEVVEAKAGKGSATLSMAYAGAV :  60

                    *        80         *       100         *       120
LpMDHa : FGDACLKGLNGVPDIVECSYVQSTITELPFFASKVRLGKNGVEEVLGLGELSAFEKEGLE : 120

                    *       140
LpMDHa : SLKGELKSSIDKGIAFANAS : 140
```

Figure 13 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHa

```
                      *        20         *        40         *        60
LpMDHa1 : GTTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  60
LpMDHa2 : -GGTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  59
LpMDHa3 : -GTGGTCTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  59
LpMDHa4 : ----GGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  56
LpMDHa5 : ------------------------------------------------------------ :   -
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                      *        80         *       100         *       120
LpMDHa1 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 120
LpMDHa2 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 119
LpMDHa3 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 119
LpMDHa4 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 116
LpMDHa5 : -------------------------------------------GAGGGTGGGACAGAAGT :  17
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                      *       140         *       160         *       180
LpMDHa1 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 180
LpMDHa2 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 179
LpMDHa3 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 179
LpMDHa4 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 176
LpMDHa5 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :  77
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                      *       200         *       220         *       240
LpMDHa1 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 240
LpMDHa2 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 239
LpMDHa3 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 239
LpMDHa4 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 236
LpMDHa5 : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 137
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                      *       260         *       280         *       300
LpMDHa1 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 300
LpMDHa2 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 299
LpMDHa3 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 299
LpMDHa4 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 296
LpMDHa5 : TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 197
LpMDHa6 : -------------------------------------------GTNANGCTCGGNNAGAA :  17
LpMDHa7 : ----------------------------------------------------------AA :   2

                      *       320         *       340         *       360
LpMDHa1 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 360
LpMDHa2 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 359
LpMDHa3 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 359
LpMDHa4 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 356
LpMDHa5 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGANAAGGAAGGTTTGGA : 257
LpMDHa6 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :  77
LpMDHa7 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :  62
```

```
                 *      380        *      400        *      420
LpMDHa1 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 420
LpMDHa2 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 419
LpMDHa3 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 419
LpMDHa4 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 416
LpMDHa5 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 317
LpMDHa6 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 137
LpMDHa7 : AAGTCTCAAGGGTGAGNTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 122

                 *      440        *      460        *      480
LpMDHa1 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT : 475
LpMDHa2 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT : 474
LpMDHa3 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT : 474
LpMDHa4 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--NTT : 471
LpMDHa5 : TTGATTAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 377
LpMDHa6 : TTGATTAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 197
LpMDHa7 : TTGATTAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 182

                 *      500        *      520        *      540
LpMDHa1 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 535
LpMDHa2 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 534
LpMDHa3 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 534
LpMDHa4 : TTGNTCANNGCTTTTTCTGCCCATCACGTGNGCATGNAAGATTTGAGCTTNACANTANNT : 531
LpMDHa5 : TTGTTCAGNGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 437
LpMDHa6 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 257
LpMDHa7 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 242

                 *      560        *      580        *      600
LpMDHa1 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 595
LpMDHa2 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 594
LpMDHa3 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 594
LpMDHa4 : ATNCCNGCGCGNN----------------------------------------------- : 544
LpMDHa5 : ATCCGGCGGCGTAATGCCACANAACATTACTTGGACAAGAGGGAACTAGTTCGGGTNAAG : 497
LpMDHa6 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 317
LpMDHa7 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 302

                 *      620        *      640        *      660
LpMDHa1 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAN----- : 650
LpMDHa2 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAA----- : 649
LpMDHa3 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAA----- : 649
LpMDHa4 : ------------------------------------------------------------ :   -
LpMDHa5 : TTTTGAACTGGNACATTAAACAAACCAATTGNTGTCGCGCTTTGNGAACCGGCCTTTGGGG : 557
LpMDHa6 : TTTTGAACTGGTACATTAAACGAACAATTGTTGATGCACTTTGTGAACCGTCCTTTGGTG : 377
LpMDHa7 : TTTTGAACTGGTACATTAAACGAACAATTGTTGAAAAAAAAAA----------------- : 345

                 *      680        *
LpMDHa1 : ------------------------------------ :   -
LpMDHa2 : ------------------------------------ :   -
LpMDHa3 : ------------------------------------ :   -
LpMDHa4 : ------------------------------------ :   -
LpMDHa5 : GTGANTCCATTGGNCTNAAGCCNAAAAAAAAA---- : 589
LpMDHa6 : TTGATTCCATTGTCTTCAAGTTAACGAANAANAAAA : 413
LpMDHa7 : ------------------------------------ :   -
```

ure 14 Consensus contig nucleotide sequence of LpMDHb

```
                    *        20         *        40         *        60
LpMDHb : TTTGGTNCTTTTGCCGAGCGAGAAAGCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGC :  60

                    *        80         *       100         *       120
LpMDHb : TAAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGT : 120

                    *       140         *       160         *       180
LpMDHb : TGGTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAA : 180

                    *       200         *       220         *       240
LpMDHb : TGCATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGA : 240

                    *       260         *       280         *       300
LpMDHb : AGTTGTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGC : 300

                    *       320         *       340         *       360
LpMDHb : AGTATTTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTC : 360

                    *       380         *       400         *       420
LpMDHb : CTTTGTGCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAA : 420

                    *       440         *       460         *       480
LpMDHb : GAACGGAGTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCT : 480

                    *       500         *       520         *       540
LpMDHb : GGAGAGCCTCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGA : 540

                    *       560         *       580         *       600
LpMDHb : GAGCTAGTCAACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGA : 600

                    *       620         *       640         *       660
LpMDHb : ATTTTTGGTACGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGNGCTC : 660

                    *       680         *       700         *       720
LpMDHb : CACAATAAAATGGCGTGNCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGT : 720

                    *       740         *       760         *       780
LpMDHb : GAAACCCTGTGCCTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAA : 780

                    *       800
LpMDHb : GATTCTGTGGAAGCTTTTTTCTTTTAN : 807
```

Figure 15 Deduced amino acid sequence of LpMDHb

```
                   *        20         *        40         *        60
LpMDHb : LXLLPSEKAVRCHHPXVVRAKTFYAGKANVPVTGVNVPVVGGHAGVTILPQFSQATPASN :  60

                   *        80         *       100         *       120
LpMDHb : ALSHEDLKALTKRTQDGGTEVVEAKAGKGSATLSMAYAGAVFGDACLKGLNGVPDIVECS : 120

                   *       140         *       160         *       180
LpMDHb : FVQSTVTELPFFASKVRLGKNGVEEVIGLGELSAFEKEGLESLKGELXXSIEKGIKFAQE : 180

LpMDHb : S : 181
```

Figure 16 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHb

```
                 *       20         *       40         *       60
LpMDHb1 : TTTGGTNCTTTTGCCGAG-NANTAATCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGCT :  60
LpMDHb2 : -----------------GCGAGAGAGCTGTTTGGTGTCACCACCCTTGTGTTGTTCGTGCT :  44

                *       80         *      100         *      120
LpMDHb1 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGTTG : 121
LpMDHb2 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCGGTCACTGGGGTGAATGTTCCTGTTGTTG : 105

               *      140         *      160         *      180
LpMDHb1 : GTGGCCATGCTGGTGTTACTATCCTGCCACTGTTCTCACAGGCTACTCCTGCAAGTAATGC : 182
LpMDHb2 : GTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC : 166

              *      200         *      220         *      240
LpMDHb1 : ATTGTCCCATGAGGATCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 243
LpMDHb2 : ATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 227

             *      260         *      280         *      300
LpMDHb1 : GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGCAGTAT : 304
LpMDHb2 : GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCGATGGCATATGCTGGTGCAGTTT : 288

            *      320         *      340         *      360
LpMDHb1 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 365
LpMDHb2 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 349

           *      380         *      400         *      420
LpMDHb1 : GCAATCAACTGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 426
LpMDHb2 : GCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 410

          *      440         *      460         *      480
LpMDHb1 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 487
LpMDHb2 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 471

         *      500         *      520         *      540
LpMDHb1 : TCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC : 548
LpMDHb2 : TCAAGGGCGAGCTGGTGTCCTCCATTGAGAAGGGTATCAAGTTCGCTCAGGAGAGCTAGTC : 532

        *      560         *      580         *      600         *
LpMDHb1 : AACCTGCTCAGATTCTGACACTCCGTACATGAACTCGGTGGGATCTGATGAATTTTTGGTA : 609
LpMDHb2 : AACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGAATTTTTGGTT : 593

              620         *      640         *      660         *
LpMDHb1 : CGACTCCTTTCTCTGCCCCTTTTTCGTGGGGACATTGAGGCGTTGNGCTTCACATTAAAAT : 670
LpMDHb2 : CGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGTGCTCCACAATAAAAT : 654

             680         *      700         *      720         *
LpMDHb1 : GGCGTGNTTTGTTG-CATACTGANCTGAGCTTNTATTCN---------------------- : 708
LpMDHb2 : GGCGTGTCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGTGAAACCCTGTGC : 715
```

```
                740         *        760         *        780         *
LpMDHb1 : ------------------------------------------------------------- :   -
LpMDHb2 : CTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAAGATTCTGTGGAAG : 776

                800
LpMDHb1 : -------------- :   -
LpMDHb2 : CTTTTTTCTTTTAN : 790
```

Figure 17 Nucleotide sequence of LpMDHc

```
                   *        20         *        40         *        60
LpMDHc : GNNGGTNTACCGAGCGCNCATACTTTNGTGGGTGAGGTTCTTGGACTNGACCCAAGAGAT :  60

                   *        80         *       100         *       120
LpMDHc : GTCAATGTTCCTGTNGNTGGCGGGCATGCCGGAGTTACNATATTGCCACTCCTTTCGCAG : 120

                   *       140         *       160         *       180
LpMDHc : GTTAATCCTCCCTGCTCATTCACCATGAGGAAATTAGTATCTCACCTTCACAGCATACAG : 180

                   *       200         *       220         *       240
LpMDHc : AATGGTGGGACAGAAGTNGTCGAGGCGAAAGCTGGAGCAGGATCGGNNACTNTTTCTATG : 240

                   *       260         *       280         *       300
LpMDHc : GCGNATGCGGCAGCTAAATTTGCAGATGCTTGCTNGAGAGGATTGCATGGTGATGCTGGG : 300

                   *       320         *       340         *       360
LpMDHc : ATAGNGGANTGCTCTTATGTGGATTCTCAGGTGACGGANCTNTCTTTNTTTGCATCCAAA : 360

                   *       380         *       400         *
LpMDHc : GTTCGCCTTGGTTGTTCTGGCGTCNAGGAGATCTTGCCACTTGGTCCACTCAACGAGTN : 419
```

Figure 18 Deduced amino acid sequence of LpMDHc

```
                    *         20         *         40         *         60
LpMDHc : XGXPSXHTXVGEVLGXDPRDVNVPXXGGHAGVXILPLLSQVNPPCSFTMRKLVSHLHSIQ :  60

                    *         80         *        100         *        120
LpMDHc : NGGTEXVEAKAGAGSXTXSMAXAAAKFADACXRGLHGDAGIXXCSYVDSQVTXXSXFASK : 120

                    *
LpMDHc : VRLGCSGVXEILPLGPLNE : 139
```

ure 19   Nucleotide sequence of LpMDHd

```
                   *        20         *        40         *        60
LpMDHd : GNGNTTCCGCCAACACAACACCACCGCTCCCCGTCCGCATCTCTCCCTTTCGCCTCCAT :  60

                   *        80         *       100         *       120
LpMDHd : CGATCCAGATCCCACACACCGCCGCAGCCAGCAACGATGAGGCCGTCGGCGATGAGATCC : 120

                   *       140         *       160         *       180
LpMDHd : GCCGCGCAGCTCCTCCGCCGCCGCAGCTACTCGTCCGCGTCCGGCCAGCCGGAGCGGAAG : 180

                   *       200         *       220         *       240
LpMDHd : GTGGCCATCCTCGGCGCGGCCGGCGGGATCGGGCAGCCGCTGGCGCTCCTCATGAAGCTG : 240

                   *       260         *       280         *       300
LpMDHd : AACCCGCTCGTCTCCTCCCTCTCCCTCTACGACATCGCCGCCACCCCCGGCGTCGCCGCC : 300

                   *       320         *       340         *       360
LpMDHd : GACGTCTCCCACATCAACTCCCCGGCCCTGGTGAAGGGGTTCATGGGCGACGATCAGCTC : 360

                   *       380         *       400         *       420
LpMDHd : GCGGAGGCGTTGGAGGGGGCCGACCTCGTCATCATCCCGGCCGGCGTTCCGAGGAAGCCC : 420

                   *       440         *       460         *       480
LpMDHd : GGCATGACCAGGGACGATCTCTTCAACATCAACGCCGGCATCGTTAAGAACCTCTGCACC : 480

                   *       500         *       520         *       540
LpMDHd : GCCATCGCCAAGTACTGCCCCAACGCTCTTATCAACATGATCAGCAACCCTGTGAACTCA : 540

                   *       560         *       580         *       600
LpMDHd : ACTGTTCCAATTGCTGCTGAAGTTTTCAAGAAGGCTGGAACCTATGATGAGAAGAAGTTG : 600

                   *       620         *       640         *       660
LpMDHd : TTTGGTGTGACCACTCTTGATGTTGTTCGTGCCAGGACTTTCTATGCTGGGAAGGCTAAT : 660

                   *       680         *       700         *       720
LpMDHd : GTACCTGTTACTGGTGTGAACGTTCCTGTTGTTGGTGGTCATGCTGGTATCACCATTCTG : 720

                   *       740         *       760         *
LpMDHd : CCACTGTTCTCACAGGCAACTCCTTCGACTAATGCATTGTCTAGTGAAGACATN : 774
```

Figure 20 Deduced amino acid sequence of LpMDHd

```
                       *        20         *        40         *        60
LpMDHd : XXPPTQHHRSPVRISPFRLHRSRSHTPPQPATMRPSAMRSAAQLLRRRSYSSASGQPERK :  60

                       *        80         *       100         *       120
LpMDHd : VAILGAAGGIGQPLALLMKLNPLVSSLSLYDIAATPGVAADVSHINSPALVKGFMGDDQL : 120

                       *       140         *       160         *       180
LpMDHd : AEALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKNLCTAIAKYCPNALINMISNPVNS : 180

                       *       200         *       220         *       240
LpMDHd : TVPIAAEVFKKAGTYDEKKLFGVTTLDVVRARTFYAGKANVPVTGVNVPVVGGHAGITIL : 240

                       *
LpMDHd : PLFSQATPSTNALSSEDX : 258
```

ure 21   Nucleotide sequence of LpMDHe

```
                 *        20         *        40         *        60
LpMDHe : TCCGTACNATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATCCTAAGAGATTGT :  60

                 *        80         *       100         *       120
LpMDHe : TGGGGGTGACAACACTTGATGTAGTGAGAGCCAATACTTTTGTGGGTGAGGTTCTTGGAC : 120

                 *       140         *       160         *       180
LpMDHe : TTGACCCCAGAGATGTCAATGTTCCTGTTGTTGGCGGGCATGCCGGAGTTACGATATTAC : 180

                 *       200         *       220         *       240
LpMDHe : CACTCCTTTCGCAGGTTAGTCCTCCCTGCTCGTTCACCCCTGAGGAAATTAGTTATCTCA : 240

                 *       260         *       280         *       300
LpMDHe : CCTCACGCATACAGAATGGTGGGACAGAAGTTGTGGAGGCGAAAGCAGGAGCAGGATCGG : 300

                 *       320         *       340         *       360
LpMDHe : CAACTCTTTCTATGGCGTATGCGGCAGCTAAATTTGCAGATGCTTGCTTGAGAGGATTGC : 360

                 *       380         *       400         *       420
LpMDHe : ATGGTGATGCTGGGATAGTGGAGTGCTCTTATGTGGATTCTCAGGTGACCGGAACTGCCT : 420

                 *       440         *       460         *       480
LpMDHe : TCTTTGCATCCAAAGTTCGCCTAGGTCGTTCTGGCGTCGAGGAGATCTTGCAACTTGGGT : 480

                 *       500         *       520         *       540
LpMDHe : CCACTGAACCAGGTTTTGAAAGANCTGGACTGGAANAAGGCGAAANAANGAGCTATCCCG : 540

                 *       560         *       580         *       600
LpMDHe : AGAGCCTTCCAGAAAGGNTGTGTCATTTCGTNCAACAAAGTGAGTTACATGCCATCATCT : 600

                 *       620         *       640         *       660
LpMDHe : TTGTTGGATGTGCTTCCCCAAAGTTCCAACACACCGTCGNAATTGGCATATANATATTGC : 660

                 *       680         *       700         *       720
LpMDHe : TGGTTTGGGGCCTTTTGCNTTNATGCAAACAGGCTACCTTNTGGGTGGGGGGGTCCGTT : 720

                 *       740         *       760         *       780
LpMDHe : NTGAAAAACTCTTAACATTTTTTTTTACGGTTGGNAACAAAATNTNTGAAAAGCCTGAGA : 780

                 *       800         *
LpMDHe : ANTATATGATAANTGAANAAAGTTTNNAAAAAAAAN : 816
```

Figure 22 Deduced amino acid sequence of LpMDHe

```
                  *        20         *        40         *        60
LpMDHe : RXIAAEVFKKAGTYNPKRLLGVTTLDVVRANTFVGEVLGLDPRDVNVPVVGGHAGVTILP :  60

                  *        80         *       100         *       120
LpMDHe : LLSQVSPPCSFTPEEISYLTSRIQNGGTEVVEAKAGAGSATLSMAYAAAKFADACLRGLH : 120

                  *       140         *       160         *       180
LpMDHe : GDAGIVECSYVDSQVTGTAFFASKVRLGRSGVEEILQLGSTEPGFERXGLEXGEXXSYPE : 180

                  *       200         *       220         *       240
LpMDHe : SLPERXCHFXQQSELHAIIFVGCASPKFQHTVXIGIXILLVWGLLXXCKQATXWVGGVRX : 240

                  *       260         *
LpMDHe : EKLLTFFFTVXNKXXEKPEXYMIXEXSXXXKK : 271
```

Figure 23 Consensus contig nucleotide sequence of LpMDHf

```
                      *        20         *        40         *        60
LpMDHf : GGGATGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC :  60

                      *        80         *       100         *       120
LpMDHf : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120

                      *       140         *       160         *       180
LpMDHf : ATTGCGGCAGAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 180

                      *       200         *       220         *       240
LpMDHf : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGNTGATCCT : 240

                      *       260         *       280         *       300
LpMDHf : AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG : 300

                      *       320         *       340         *       360
LpMDHf : NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 360

                      *       380         *       400         *       420
LpMDHf : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 420

                      *       440         *       460         *       480
LpMDHf : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 480

                      *       500         *       520         *       540
LpMDHf : GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA : 540

                      *       560         *       580         *       600
LpMDHf : ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGGCCACTGAAT : 600

                      *       620         *       640         *       660
LpMDHf : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG : 660

                      *       680         *       700         *       720
LpMDHf : GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCCGCAACCTATAC : 720

                      *       740         *       760         *       780
LpMDHf : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT : 780

                      *
LpMDHf : CTCTCCTGCCTGTAAGAA : 798
```

Figure 24 Deduced amino acid sequence of LpMDHf

```
                    *        20         *        40         *        60
LpMDHf : MLGIVRSICEGVAKSCPNAIVNLISNPVNSTVPIAAEXFKRAGTYCPKRLLGVTTLDVAR :  60

                    *        80         *       100         *       120
LpMDHf : ANTFVAEVLGXDPREXSVPXVGGHAGITILPLLXQVSPPCSFTPDEISYLTNRIQNGGTE : 120

                    *       140         *       160         *       180
LpMDHf : VVEAKAGAGSATLSMAFAAAKFADACLRGMRGDAGIVECXYVASEVTELPFFATKVRLGR : 180

                    *       200         *       220
LpMDHf : GGAEEILPLGPLNDFERAGLEKAXKELSESIQKGVAFMNK : 220
```

gure 25   Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHf

```
                    *        20         *        40         *        60
LpMDHf1 : GNNNTGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC :  60
LpMDHf2 : -GGATGATTTATTCAACAAAAATGCTGGG-ATTGTCCGATCAATCTGTGAGGGCGTTGCC :  58

                    *        80         *       100         *       120
LpMDHf1 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120
LpMDHf2 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 118

                    *       140         *       160         *       180
LpMDHf1 : ATTGCGGCANAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 180
LpMDHf2 : ATTGCGGCAGAAGTTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 178

                    *       200         *       220         *       240
LpMDHf1 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGNAGNTGATCCT : 240
LpMDHf2 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGTTGATCCT : 238

                    *       260         *       280         *       300
LpMDHf1 : AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCNGGGATCACTATATTGCCCCTCCTG : 300
LpMDHf2 : AGAGAAGTCAGTGTTCCGGTTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG : 298

                    *       320         *       340         *       360
LpMDHf1 : NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 360
LpMDHf2 : TCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 358

                    *       380         *       400         *       420
LpMDHf1 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 420
LpMDHf2 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 418

                    *       440         *       460         *       480
LpMDHf1 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 480
LpMDHf2 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 478

                    *       500         *       520         *       540
LpMDHf1 : GCTGGCATTGTGGAATGTTCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA : 540
LpMDHf2 : GCTGGNATTGTGGAATGTN----------------------------------------- : 497

                    *       560         *       580         *       600
LpMDHf1 : ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGGCCACTGAAT : 600
LpMDHf2 : ------------------------------------------------------------ :   -

                    *       620         *       640         *       660
LpMDHf1 : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG : 660
LpMDHf2 : ------------------------------------------------------------ :   -

                    *       680         *       700         *       720
LpMDHf1 : GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCCGCAACCTATAC : 720
LpMDHf2 : ------------------------------------------------------------ :   -
```

```
                  *       740        *       760        *       780
LpMDHf1 : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT : 780
LpMDHf2 : ------------------------------------------------------------ :   -

                  *
LpMDHf1 : CTCTCCTGCCTGTAAGAA : 798
LpMDHf2 : ------------------ :   -
```

Figure 26 Nucleotide sequence of LpMDHg

```
                  *        20         *        40         *        60
LpMDHg : CAATTGCACGTTCTTGCTCACTTCAGCATCACCCTCACGCTTCTCCTACACAACCCCTCC :  60

                  *        80         *       100         *       120
LpMDHg : CAACCGTCACTATGGTCAAGGCTGTCGTCGCAGGTGCTGCTGGTGGTATCGGCCAGCCCC : 120

                  *       140         *       160         *       180
LpMDHg : TCTCTCTTCTACTCAAGACGAGCCCCCTCATCGATGAGCTTGCCCTCTACGATGTTGTCA : 180

                  *       200         *       220         *       240
LpMDHg : ACACTCCCGGTGTTGCCGCTGATCTTTCCCACATCTCATCCCGCGCTCAAATCGCCGGCT : 240

                  *       260         *       280         *       300
LpMDHg : ACCTCCCCAAGGATGATGGCGCAAAGGCTGCATTCAAAGATGCCGACATTATCGTCATCC : 300

                  *       320         *       340         *       360
LpMDHg : CCGCCGGCATTCCTCGCAAGCCTGGCATGACCCGTGATGACCTCTTCAACATCAACGCCG : 360

                  *       380         *       400         *       420
LpMDHg : GAATTGTCAAGGGTCTGATTGAGGTTGCCGCCGAAGTTGCCCCCAAGGCCTTCATTCTGG : 420

                  *       440         *       460         *       480
LpMDHg : TCATCTCCAACCCTGTCAACTCTACCGTCCCTATCTCTGCCGAGGTCCTCAAGGCCAAGG : 480

                  *       500         *       520         *       540
LpMDHg : GCGTCTTCAACCCTCAGCGTCTTTTCGGTGTCACCACCCTCGACATCGTCCGTGCCGAGA : 540

                  *       560         *       580         *       600
LpMDHg : CTTTCGTCGCCAGCATCACCGGCGAGAAGCAGCCCCAGAACTTGACCGTCCCCGTCATTG : 600

                  *       620         *       640         *       660
LpMDHg : GCGGCCACTCCGGCGAGACCATCGTCCCGCTTTTCAGCAAGGNTCAGCCCTCTGCTTNCA : 660

LpMDHg : TTCCCGC : 667
```

Figure 27 Deduced amino acid sequence of LpMDHg

```
                   *        20         *        40         *        60
LpMDHg : IARSCSLQHHPHASPTQPLPTVTMVKAVVAGAAGGIGQPLSLLLKTSPLIDELALYDVVN :  60

                   *        80         *       100         *       120
LpMDHg : TPGVAADLSHISSRAQIAGYLPKDDGAKAAFKDADIIVIPAGIPRKPGMTRDDLFNINAG : 120

                   *       140         *       160         *       180
LpMDHg : IVKGLIEVAAEVAPKAFILVISNPVNSTVPISAEVLKAKGVFNPQRLFGVTTLDIVRAET : 180

                   *       200         *       220
LpMDHg : FVASITGEKQPQNLTVPVIGGHSGETIVPLFSKXQPSAXIP : 221
```

Figure 28 Consensus contig nucleotide sequence of LpMDHh

```
                         *        20         *        40         *        60
LpMDHh : TNACGGAGCTGCTTAAATCAGCCCCCATTCCGCCTCGTCTATAGCGATCCTTCATCCCGT :  60

                         *        80         *       100         *       120
LpMDHh : TGTCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATG : 120

                         *       140         *       160         *       180
LpMDHh : GCGGCGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCT : 180

                         *       200         *       220         *       240
LpMDHh : CTTGTTCCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCAT : 240

                         *       260         *       280         *       300
LpMDHh : ATGCTGGATATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGAT : 300

                         *       320         *       340         *       360
LpMDHh : GCCGCATTTCCACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACT : 360

                         *       380         *       400         *       420
LpMDHh : GGTGTGAATGTTGCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAG : 420

                         *       440         *       460         *       480
LpMDHh : GATGTTATGTCTAAGAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCAT : 480

                         *       500         *       520         *       540
LpMDHh : GCAGCCCCGAATTGCAAGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATC : 540

                         *       560         *       580         *       600
LpMDHh : TTAAAGGAGTTTGCTCCATCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGAC : 600

                         *       620         *       640         *       660
LpMDHh : CATAACAGGGCACTTGGTCAGATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAG : 660

                         *       680         *       700         *       720
LpMDHh : AATGTTATCATCTGGGGCAATCACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACC : 720

                         *       740         *       760         *       780
LpMDHh : GTGAAGACTTCCAGTGGCGAGAAGCCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTA : 780

                         *       800         *       820         *       840
LpMDHh : AATGCAGGGTTCATTGCCACTGTCCAGCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAG : 840

                         *       860         *       880         *       900
LpMDHh : CTCTCCAGTGCTCTCTCTGCTGCCAGCTCTGCTTGTGACCACATCCGTGATTGGGTTCTC : 900

                         *       920         *       940         *       960
LpMDHh : GGAACCCCTGAGGGAACATTTGTTTCCATGGGTGTGTATTCTGATGGTTCATACGGTGTG : 960
```

```
                    *        980          *        1000          *        1020
LpMDHh : CCTGCTGGGCTTATCTACTCCTTCCCAGTAACTTGCTGCGGTGGTGAATGGACAATTGTT : 1020

                    *       1040          *        1060          *        1080
LpMDHh : CAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGAAGATGGATGCCACAGCCCAGGAGCTC : 1080

                    *       1100          *        1120          *        1140
LpMDHh : TCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAGTAACTGCATACCAGGGAGCAGCTG : 1140

                    *       1160          *        1180          *        1200
LpMDHh : CCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTCCATGAAACTCATCTCCACTCAG : 1200

                    *       1220          *        1240          *        1260
LpMDHh : AACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAGTGTGTATGAATGAGGCTTTT : 1260

                    *       1280          *        1300          *        1320
LpMDHh : GTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTGGCAGGAAGATTGGAACAA : 1320

                    *       1340          *        1360          *        1380
LpMDHh : TTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTATGAATGAGGCTTTTGT : 1380

                    *       1400          *        1420          *        1440
LpMDHh : AGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGAGGATTGGAACAATT : 1440

                    *       1460          *        1480
LpMDHh : TGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAAAAA : 1484
```

Figure 29 Deduced amino acid sequence of LpMDHh

```
                  *        20         *        40         *        60
LpMDHh : MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEALNGVKMELV :  60

                  *        80         *       100         *       120
LpMDHh : DAAFPLLKGVVATTDVVEACTGVNVAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEA : 120

                  *       140         *       160         *       180
LpMDHh : HAAPNCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLDVQVSDV : 180

                  *       200         *       220         *       240
LpMDHh : KNVIIWGNHSSSQYPDVNHATVKTSSGEKPVRELVKDDEWLNAGFIATVQQRGAAIIKAR : 240

                  *       260         *       280         *       300
LpMDHh : KLSSALSAASSACDHIRDWVLGTPEGTFVSMGVYSDGSYGVPAGLIYSFPVTCCGGEWTI : 300

                  *       320         *
LpMDHh : VQGLPIDEFSRKKMDATAQELSEEKALAYSCLE : 333
```

Figure 30 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHh

```
                    *        20         *        40         *        60
LpMDHh1  : TNACGGAGCTGCTTAAATCAGCCCCCATTCCGCCTCGTCT-C-ACTATCCTTCATCCCGTTG : 60
LpMDHh2  : ----------------------------GGGNTTTTAGCTGT-NCNAN-CC-CGTGNCGTT- : 29
LpMDHh3  : ------------------------------------GNGTAT-GCTNTGNTACA-CGNTGTN : 24
LpMDHh4  : --------------------------------------GTTTACCGTTNCTAC--CNNTGTN : 22
LpMDHh5  : ------------------------------------------GNNTACCTTNCTNCCCGTTG : 20
LpMDHh6  : -------------------------------------------GNNTNCCTTNCTCCCGTTG : 19
LpMDHh7  : -------------------------------------------GCTTT-CCTTATCCCGTTG : 18
LpMDHh8  : -------------------------------------------GCTATCCTTCATCCCGTTG : 19
LpMDHh9  : -------------------------------------------GCTATCCTTCATCCCGTTG : 19
LpMDHh10 : --------------------------------------------NTAGCTTNCTNCCCGTTG : 18
LpMDHh11 : --------------------------------------------GNNTACCTTCTCCCCGTG : 18
LpMDHh12 : --------------------------------------------CTATCCTT-ATCCCGTTG : 17
LpMDHh13 : ---------------------------------------------GATCCTT-ATCCCGTTG : 16
LpMDHh14 : ---------------------------------------------GNNACCTTCTCCCGTTG : 17
LpMDHh15 : ---------------------------------------------GATCCTTCATCCCGTTG : 17
LpMDHh16 : ---------------------------------------------GNTCCTTCATCCCGTTG : 17
LpMDHh17 : ---------------------------------------------GATCCTT-ATCCCGTTG : 16
LpMDHh18 : ---------------------------------------------GNTCCGTCATCCCGTTG : 17
LpMDHh19 : ---------------------------------------------GNNCCTTCATCCCGTTG : 17
LpMDHh20 : ---------------------------------------------GNTCCTT-NTCCCGTTG : 16
LpMDHh21 : ---------------------------------------------GNTCCTTCATCCCGTTG : 17
LpMDHh22 : ---------------------------------------------GATCCTTCATCCCGTTG : 17
LpMDHh23 : ----------------------------------------------GNCCTTNATCCCNTTG : 16
LpMDHh24 : ----------------------------------------------GNTCCTTATCCCGTTG : 16
LpMDHh25 : ----------------------------------------------TTCCTTNCTCCCGTTG : 16
LpMDHh26 : -----------------------------------------------TCCTTNATCCCGTTG : 15
LpMDHh27 : -----------------------------------------------ACCTTCTNCCCGTTG : 15
LpMDHh28 : -----------------------------------------------TCCTT-NTCCCGTTG : 14
LpMDHh29 : -----------------------------------------------TCCTT-ATCCCGTTG : 14
LpMDHh30 : -----------------------------------------------TCCTTCNTCCCGTTG : 15
LpMDHh31 : ------------------------------------------------CCTTCATCCCGTTG : 14
LpMDHh32 : ------------------------------------------------NCGTTGTCCCNTTG : 14
LpMDHh34 : ------------------------------------------------ACCTTATCCCGTTG : 14
LpMDHh35 : -------------------------------------------------CTTNCTCCCGTTG : 13
LpMDHh36 : -------------------------------------------------TTNCTNCCGNCTG : 13
LpMDHh37 : -------------------------------------------------TTNCTNCCCCCNG : 13
LpMDHh38 : -------------------------------------------------NTTCATCCCGTTG : 13
LpMDHh39 : --------------------------------------------------TTCATCCCNTTG : 12
LpMDHh40 : --------------------------------------------------TTGATCCCGTTG : 12
LpMDHh41 : --------------------------------------------------NTTATCCCGGTG : 12
LpMDHh42 : --------------------------------------------------NTTATCCCGTTG : 12
LpMDHh43 : --------------------------------------------------GTCNTCCCGTTG : 12
LpMDHh44 : --------------------------------------------------TT-NTCCCGTTG : 11
LpMDHh45 : ---------------------------------------------------TTCTCCCGTTG : 11
LpMDHh46 : ---------------------------------------------------TTGTCCCGTTG : 11
LpMDHh47 : ------------------------------------------------------TCCCGTTG : 8
LpMDHh48 : --------------------------------------------------------CG-TTG : 5
LpMDHh49 : --------------------------------------------------------CCGTTG : 6
LpMDHh50 : -------------------------------------------------------------- : -
LpMDHh51 : -------------------------------------------------------------- : -
LpMDHh52 : -------------------------------------------------------------- : -
LpMDHh53 : -------------------------------------------------------------- : -
LpMDHh54 : -------------------------------------------------------------- : -
LpMDHh55 : -------------------------------------------------------------- : -
LpMDHh56 : -------------------------------------------------------------- : -
LpMDHh57 : -------------------------------------------------------------- : -
LpMDHh58 : -------------------------------------------------------------- : -
LpMDHh59 : -------------------------------------------------------------- : -
LpMDHh60 : -------------------------------------------------------------- : -
LpMDHh61 : -------------------------------------------------------------- : -
LpMDHh62 : -------------------------------------------------------------- : -
LpMDHh63 : -------------------------------------------------------------- : -
LpMDHh64 : -------------------------------------------------------------- : -
```

```
                      *       80         *        100         *        120
LpMDHh1  : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG : 122
LpMDHh2  : T-G-CTNCTGCGCGN-AACCACTCTCCCCANCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  88
LpMDHh3  : CGTTCGCCTCCTCCCGACCCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  86
LpMDHh4  : CGTTCGCCTCCTCCCG-AAAACNCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  83
LpMDHh5  : TCGTCGCCTCCTCCCGAACCACTCTNCCCNNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  82
LpMDHh6  : TCGTCGCCTCCTCCCGANCCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  80
LpMDHh7  : TCG-CTNCTCCTCCC-GACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh8  : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  81
LpMDHh9  : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  81
LpMDHh10 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  79
LpMDHh11 : TCGTCACCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  80
LpMDHh12 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh13 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh14 : TCGTCGCCTCCTCCCGNACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh15 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh16 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh17 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh18 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh19 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh20 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh21 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh22 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh23 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh24 : TCGTCGNCTNCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh25 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh26 : TCGTCGCCTCCTCCCGAACC-CTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh27 : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh28 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh29 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh30 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh31 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh32 : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh34 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAACGGCGG :  75
LpMDHh35 : TCGTCGCCTCCTCCCGAACCACTCTCCCCTNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh36 : TCGTCGCCTCCTCCCGAACCACTCTCCCCTNCCCCGAACTCCA-AACCGGCTCCAATGGCGG :  74
LpMDHh37 : TCGTCGCCTCCTCCCGAACCACTCTCCCCNNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh38 : TCGTCGCCTCCTCCCG-AACNCTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  74
LpMDHh39 : TCGTNGCCTNCTCCCGAACCACTCTCCCCTTCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  74
LpMDHh40 : TCGTCGCCTCCTCCCG-AACCCTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh41 : TCGTCGCCTCCTCCCGAACN-CTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh42 : TCGTCGCCTCCTCCCGAACC-CTCTCCCCATCCCCGAACTCC-GAACCGGCTCCAATGGCGG :  72
LpMDHh43 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh44 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  72
LpMDHh45 : TCGTCGCCTCCTCCCG-ACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  71
LpMDHh46 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  72
LpMDHh47 : TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  69
LpMDHh48 : TCGTCGCCTCCTCCCG-ACCCTNCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  65
LpMDHh49 : TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  68
LpMDHh50 : ---------------GGACC-CTCTCCCCATCCCCGAACTCCAGNACCGGCTCCAATGGCGG :  46
LpMDHh51 : ------------------------------NCCCCGNANTCCA-NACCGGCTCCAA-GGCGG :  30
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

```
                  *      140       *      160       *      180
LpMDHh1  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 184
LpMDHh2  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGTAGGACAAATTGGATATGCTCTTGTT : 150
LpMDHh3  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 148
LpMDHh4  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 145
LpMDHh5  : CGAAGNAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 144
LpMDHh6  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 142
LpMDHh7  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh8  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 143
LpMDHh9  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 143
LpMDHh10 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 141
LpMDHh11 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 142
LpMDHh12 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh13 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh14 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh15 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh16 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh17 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh18 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh19 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh20 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh21 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh22 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh23 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh24 : NGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh25 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh26 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138
LpMDHh27 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh28 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh29 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh30 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138
LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACANATTGGATATGCTCTTGTT : 138
LpMDHh34 : CNAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCNTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh43 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 133
LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131
LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127
LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130
LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108
LpMDHh51 : CGAAGNAACCGA-GCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT :  91
LpMDHh52 : -----GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGNCAAATTGGATATGCTCTTGTT :  57
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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                 *       200         *       220         *       240
LpMDHh1  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 246
LpMDHh2  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 212
LpMDHh3  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 210
LpMDHh4  : CCGATGATTGCTAGGCNAATTATGCTTGGNGTGCACTAGCCTGTTATTNTGCATATC----- : 202
LpMDHh5  : CCGATGATTGCTAGGGGAATTATGCTTGGTGTGGACCAGCCTGTTATTCTGCATATGCTGGA : 206
LpMDHh6  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 204
LpMDHh7  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh8  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 205
LpMDHh9  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 205
LpMDHh10 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 203
LpMDHh11 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 204
LpMDHh12 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh13 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh14 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh15 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh16 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh17 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh18 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh19 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh20 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh21 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh22 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh23 : CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh24 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh25 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh26 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh27 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh28 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh29 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh30 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh31 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh32 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh34 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh35 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh36 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh37 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh38 : CCGATGATTGCTAGGGGAATTATGCTCGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh39 : CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCANCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh40 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCAGGA : 197
LpMDHh41 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCCGTTATTCTGCATATGCTGGA : 197
LpMDHh42 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh43 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 197
LpMDHh44 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh45 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 195
LpMDHh46 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh47 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 193
LpMDHh48 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 189
LpMDHh49 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 192
LpMDHh50 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 170
LpMDHh51 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 153
LpMDHh52 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 119
LpMDHh53 : --------------------TATGCTTGGTGCGG-CCAGCCTGTTATTCTGCATATGCTGGA : 41
LpMDHh54 : -------------------------------------------------------------- : -
LpMDHh55 : -------------------------------------------------------------- : -
LpMDHh56 : -------------------------------------------------------------- : -
LpMDHh57 : -------------------------------------------------------------- : -
LpMDHh58 : -------------------------------------------------------------- : -
LpMDHh59 : -------------------------------------------------------------- : -
LpMDHh60 : -------------------------------------------------------------- : -
LpMDHh61 : -------------------------------------------------------------- : -
LpMDHh62 : -------------------------------------------------------------- : -
LpMDHh63 : -------------------------------------------------------------- : -
LpMDHh64 : -------------------------------------------------------------- : -
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                 *      260         *       280         *       300         *
LpMDHh1  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 308
LpMDHh2  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGNATTTN : 274
LpMDHh3  : TATTGCACCAGCTGCTGAAGCTCTTAATGGCGTTAACATGGAAGTGNNT-NGGCGGCNTAGN : 271
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 268
LpMDHh6  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 266
LpMDHh7  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh8  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 267
LpMDHh9  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 267
LpMDHh10 : TATTCCACCAGCCGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 265
LpMDHh11 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 266
LpMDHh12 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh13 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh14 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh15 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh16 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh17 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh18 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh19 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh20 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh21 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh22 : TATTCCACCAGCTGCTGAANCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh23 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCNCATTTC : 263
LpMDHh24 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh25 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh26 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh27 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh28 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh29 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh30 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh31 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh32 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh34 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh35 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh36 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh37 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh38 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh39 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh40 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGNTGATGCCGCATTTC : 259
LpMDHh41 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 259
LpMDHh42 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh43 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 259
LpMDHh44 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh45 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 257
LpMDHh46 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh47 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 255
LpMDHh48 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 251
LpMDHh49 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 254
LpMDHh50 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 232
LpMDHh51 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 215
LpMDHh52 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 181
LpMDHh53 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 103
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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                 320         *        340         *        360         *
LpMDHh1  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 370
LpMDHh2  : CACTTGTNAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGNGNGAATGT- : 335
LpMDHh3  : NCTTTNTCGCN---------------------------------------------------- : 282
LpMDHh4  : --------------------------------------------------------------- :   -
LpMDHh5  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 330
LpMDHh6  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328
LpMDHh7  : CACTTCTCAAGGGAGTTGTTGCAACAACTGACGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh8  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329
LpMDHh9  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329
LpMDHh10 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 327
LpMDHh11 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328
LpMDHh12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh13 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh14 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh15 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh16 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh17 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh18 : CACTTCTCAAGGGAGTTGTTGCGACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh20 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh21 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh22 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh23 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTNAGGCTTGCACTGG---------- : 315
LpMDHh24 : CACTTNTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh25 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh26 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh27 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh28 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh29 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh30 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322
LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGCT : 323
LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322
LpMDHh39 : CACTTCTCAAGGGAGNTGNTGCAACAACTGATGTTGNTGAGGCTNGCACTGGTGTGAATGTT : 322
LpMDHh40 : CACTTNTCAAGGGAGTTGNTGCAACAACTGATGTNGTTGANGCTTGCACTGGNGTGAATGTT : 321
LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321
LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321
LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 319
LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 317
LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 313
LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 316
LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 294
LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 277
LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 243
LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 165
LpMDHh54 : --------------------------------------------------------------- :   -
LpMDHh55 : --------------------------------------------------------------- :   -
LpMDHh56 : --------------------------------------------------------------- :   -
LpMDHh57 : --------------------------------------------------------------- :   -
LpMDHh58 : --------------------------------------------------------------- :   -
LpMDHh59 : --------------------------------------------------------------- :   -
LpMDHh60 : --------------------------------------------------------------- :   -
LpMDHh61 : --------------------------------------------------------------- :   -
LpMDHh62 : --------------------------------------------------------------- :   -
LpMDHh63 : --------------------------------------------------------------- :   -
LpMDHh64 : --------------------------------------------------------------- :   -
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              380       *       400       *       420       *
LpMDHh1  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 432
LpMDHh2  : -------------------------------------------------------------- : -
LpMDHh3  : -------------------------------------------------------------- : -
LpMDHh4  : -------------------------------------------------------------- : -
LpMDHh5  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 392
LpMDHh6  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 390
LpMDHh7  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh8  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 391
LpMDHh9  : GCGTTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 391
LpMDHh10 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 389
LpMDHh11 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 390
LpMDHh12 : GCGTTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh13 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh14 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh15 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh16 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh17 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh18 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh19 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh20 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh21 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh22 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh23 : -------------------------------------------------------------- : -
LpMDHh24 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh25 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh26 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh27 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh28 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh29 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh30 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh31 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh32 : GCGGTTATGGNTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh34 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh35 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh36 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 384
LpMDHh37 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh38 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 384
LpMDHh39 : GCGGTTATGGATGGTGGAT------------------------------------------- : 341
LpMDHh40 : GCGGNNNTGNCNNGCCCANCTAANATNN---------------------------------- : 349
LpMDHh41 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 383
LpMDHh42 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh43 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 383
LpMDHh44 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh45 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 381
LpMDHh46 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh47 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 379
LpMDHh48 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 375
LpMDHh49 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 378
LpMDHh50 : GCGGTTATGGTTGGTGGATCCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 356
LpMDHh51 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 339
LpMDHh52 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 305
LpMDHh53 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAGTGGAAAGGAAGGATGTTATGTCTAA : 227
LpMDHh54 : ------TNGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 56
LpMDHh55 : -------------------------------------------------------------- : -
LpMDHh56 : -------------------------------------------------------------- : -
LpMDHh57 : -------------------------------------------------------------- : -
LpMDHh58 : -------------------------------------------------------------- : -
LpMDHh59 : -------------------------------------------------------------- : -
LpMDHh60 : -------------------------------------------------------------- : -
LpMDHh61 : -------------------------------------------------------------- : -
LpMDHh62 : -------------------------------------------------------------- : -
LpMDHh63 : -------------------------------------------------------------- : -
LpMDHh64 : -------------------------------------------------------------- : -
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              440         *         460         *         480         *
LpMDHh1  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 494
LpMDHh2  : -------------------------------------------------------------- :  -
LpMDHh3  : -------------------------------------------------------------- :  -
LpMDHh4  : -------------------------------------------------------------- :  -
LpMDHh5  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 454
LpMDHh6  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 452
LpMDHh7  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCNAATTGCA : 450
LpMDHh8  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 453
LpMDHh9  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 453
LpMDHh10 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 451
LpMDHh11 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 452
LpMDHh12 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh13 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh14 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh15 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh16 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh17 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh18 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh19 : GAATGTTTCAATCTACAAATCTCAAGCATCCGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh20 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh21 : GAATGTTTCAATCTACAAATCTCAAGCATCCGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh22 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh23 : -------------------------------------------------------------- :  -
LpMDHh24 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh25 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh26 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh27 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh28 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh29 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh30 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh31 : NAATGTTTCAATCTACAAATCTTAAGCATCTGCCCTTGAAGCCCATGCA-CCCCNAATTGCA : 446
LpMDHh32 : NAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh34 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh35 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh36 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 446
LpMDHh37 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh38 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCATGCAGCCCCGAATTGCA : 445
LpMDHh39 : -------------------------------------------------------------- :  -
LpMDHh40 : -------------------------------------------------------------- :  -
LpMDHh41 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 445
LpMDHh42 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh43 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 445
LpMDHh44 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh45 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 443
LpMDHh46 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh47 : TAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 441
LpMDHh48 : GAATGTTTCAATCTACAAATCTCAAGTATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 437
LpMDHh49 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 440
LpMDHh50 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 418
LpMDHh51 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGTA : 401
LpMDHh52 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 367
LpMDHh53 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 289
LpMDHh54 : GAATGTTTCAATCTACAAATCTCAAGNGNNTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 118
LpMDHh55 : ----------------------TAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA :  40
LpMDHh56 : -----------------------------------------CCATGCAA-CCCCGNANTGCA :  20
LpMDHh57 : ---------------------------------------------TGCAGCCCCG-ATTGCA :  16
LpMDHh58 : -------------------------------------------------------------- :  -
LpMDHh59 : -------------------------------------------------------------- :  -
LpMDHh60 : -------------------------------------------------------------- :  -
LpMDHh61 : -------------------------------------------------------------- :  -
LpMDHh62 : -------------------------------------------------------------- :  -
LpMDHh63 : -------------------------------------------------------------- :  -
LpMDHh64 : -------------------------------------------------------------- :  -
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             500         *        520         *        540         *         5
LpMDHh1  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 556
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 516
LpMDHh6  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 514
LpMDHh7  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh8  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 515
LpMDHh9  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 515
LpMDHh10 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 513
LpMDHh11 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 514
LpMDHh12 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh13 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh14 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh15 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTCGCTCCA : 512
LpMDHh16 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh17 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh18 : AGGTTCTGGTTGTTGCCAATCCAGTAAACACCAATGCTCTTATCCTAAAGGAGTTTGCTCCA : 512
LpMDHh19 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh20 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh21 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTNTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh22 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATNTTAAAGGAGTTTGCTCCA : 511
LpMDHh25 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh26 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh27 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh28 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh29 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh30 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh31 : AGGGTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTTTTATTTTAAANGAGTTTGCTCCA : 508
LpMDHh32 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCANTGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh34 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh35 : AGGTTCTGGTTGTTGCCAATCCA--------------------------------------- : 470
LpMDHh36 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 508
LpMDHh37 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh38 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 507
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGNTTGCTCCA : 507
LpMDHh42 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh43 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 507
LpMDHh44 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh45 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 505
LpMDHh46 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh47 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTTTTATCTTAAAGGAGTTTGCTCCA : 503
LpMDHh48 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 499
LpMDHh49 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 502
LpMDHh50 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 480
LpMDHh51 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 463
LpMDHh52 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 429
LpMDHh53 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 351
LpMDHh54 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 180
LpMDHh55 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 102
LpMDHh56 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :  82
LpMDHh57 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :  78
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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		60 * 580 * 600 * 620		
LpMDHh1	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	618
LpMDHh2	:	--	:	-
LpMDHh3	:	--	:	-
LpMDHh4	:	--	:	-
LpMDHh5	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	578
LpMDHh6	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	576
LpMDHh7	:	TCTATTCCTGANAAGAACATNAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTNGGTCA	:	574
LpMDHh8	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	577
LpMDHh9	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	577
LpMDHh10	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	575
LpMDHh11	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	576
LpMDHh12	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	574
LpMDHh13	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGc----------	:	563
LpMDHh14	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	574
LpMDHh15	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	574
LpMDHh16	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	574
LpMDHh17	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	573
LpMDHh18	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTcGGTCA	:	574
LpMDHh19	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	574
LpMDHh20	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	573
LpMDHh21	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	574
LpMDHh22	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	574
LpMDHh23	:	--	:	-
LpMDHh24	:	TCTNTTCCTGAGAA--	:	525
LpMDHh25	:	TCTATTCCTGAGAAGAACATCAGaTGTTTGACCCGNCTAGACCATAACAGGGCACTcGGTCA	:	573
LpMDHh26	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	572
LpMDHh27	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	573
LpMDHh28	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	571
LpMDHh29	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	571
LpMDHh30	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTcGGTCA	:	572
LpMDHh31	:	TNTATTCCTGANAAGAACATNANTTGTTTGACCCGCCTAGACCATAACANGGNNCTTGNcAA	:	570
LpMDHh32	:	TCTATcCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	572
LpMDHh34	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	571
LpMDHh35	:	--	:	-
LpMDHh36	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	570
LpMDHh37	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGNCTAGACCATAACAGGGCACTCGGNCA	:	571
LpMDHh38	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	569
LpMDHh39	:	--	:	-
LpMDHh40	:	--	:	-
LpMDHh41	:	TCTATTCCTGAGAANAACATCAGNTGTTTGACCCGCCTAGACCATAACAGGNCACTCGGNCA	:	569
LpMDHh42	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	568
LpMDHh43	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	569
LpMDHh44	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	568
LpMDHh45	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	567
LpMDHh46	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTcGGTCA	:	568
LpMDHh47	:	TCTATTCCTGANAAGAACATNANTTGTTTGACCCGCCTAaACCATAACAGGGCACTTGGTCA	:	565
LpMDHh48	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	561
LpMDHh49	:	TCTATTCCTGAGAAGAACATCAGTTaTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	564
LpMDHh50	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	542
LpMDHh51	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTcGGTCA	:	525
LpMDHh52	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	491
LpMDHh53	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	413
LpMDHh54	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTNA	:	242
LpMDHh55	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA	:	164
LpMDHh56	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	144
LpMDHh57	:	TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA	:	140
LpMDHh58	:	--	:	-
LpMDHh59	:	--	:	-
LpMDHh60	:	--	:	-
LpMDHh61	:	--	:	-
LpMDHh62	:	--	:	-
LpMDHh63	:	--	:	-
LpMDHh64	:	--	:	-

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                  *        640         *        660         *        680
LpMDHh1  : GATCTCTGAGAGACTTGATGNCCAAGTTAGTGATGTGAANAATGTTATCATCTGGGCAATC : 680
LpMDHh2  : ------------------------------------------------------------- :  -
LpMDHh3  : ------------------------------------------------------------- :  -
LpMDHh4  : ------------------------------------------------------------- :  -
LpMDHh5  : GATCTCTGAGAGACTTGATGGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 640
LpMDHh6  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 638
LpMDHh7  : GATCTCTGAGAGACTTNATGTCCAANTTAGTGATGTGAANAATGTTATCATCTGGGTAATC : 636
LpMDHh8  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 639
LpMDHh9  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 639
LpMDHh10 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 637
LpMDHh11 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 638
LpMDHh12 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 636
LpMDHh13 : ------------------------------------------------------------- :  -
LpMDHh14 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 636
LpMDHh15 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 636
LpMDHh16 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 636
LpMDHh17 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 635
LpMDHh18 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 636
LpMDHh19 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 636
LpMDHh20 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 635
LpMDHh21 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 636
LpMDHh22 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 636
LpMDHh23 : ------------------------------------------------------------- :  -
LpMDHh24 : ------------------------------------------------------------- :  -
LpMDHh25 : GATCTCTGAGAGACTTGATGTGCAAGTTANGGATGTGAANAATGCTATCATCTGGGANATC : 635
LpMDHh26 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAAAATGTTATCATCTGGGCAATC : 634
LpMDHh27 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 635
LpMDHh28 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 633
LpMDHh29 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 633
LpMDHh30 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 634
LpMDHh31 : AATCTTTNANAGACTTGNTNTCAAN------------------------------------ : 595
LpMDHh32 : GATCTCTGAGAGACTTGATGTCCAAGTTAGNGATGNGAANAATGTTATCATCTGGGCAATC : 634
LpMDHh34 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 633
LpMDHh35 : ------------------------------------------------------------- :  -
LpMDHh36 : GATCTCTGANAGACTTGATGTCCAAGTTA-------------------------------- : 599
LpMDHh37 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATG-------------------------- : 606
LpMDHh38 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 631
LpMDHh39 : ------------------------------------------------------------- :  -
LpMDHh40 : ------------------------------------------------------------- :  -
LpMDHh41 : GANCTCTGAGAGACNTGATGGCCAAGNTNGNGNTGN------------------------- : 605
LpMDHh42 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGCAAATC : 630
LpMDHh43 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 631
LpMDHh44 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 630
LpMDHh45 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 629
LpMDHh46 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 630
LpMDHh47 : GATCTNTGANAGACTTGATGCCCAAGTTAGNGATGTGAAAAATGTTATCATNTGGGCAATN : 627
LpMDHh48 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 623
LpMDHh49 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 626
LpMDHh50 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 604
LpMDHh51 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 587
LpMDHh52 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 553
LpMDHh53 : GATCTCTGAGAGACTTGATGTNCAAGTTAGTGATGTGAANAATGNTATCATCTGGNCANCTC : 475
LpMDHh54 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 304
LpMDHh55 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGTAATC : 226
LpMDHh56 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 206
LpMDHh57 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAATC : 202
LpMDHh58 : -------------------------------------------------------GCAATC :  6
LpMDHh59 : ------------------------------------------------------------- :  -
LpMDHh60 : ------------------------------------------------------------- :  -
LpMDHh61 : ------------------------------------------------------------- :  -
LpMDHh62 : ------------------------------------------------------------- :  -
LpMDHh63 : ------------------------------------------------------------- :  -
LpMDHh64 : ------------------------------------------------------------- :  -
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                  *     700        *       720        *      740
LpMDHh1  : ACTCTTNCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGCCGAGAAG : 742
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : ACTCTTCCAG---------------------------------------------------- : 650
LpMDHh6  : ACTCTTCCAGTCAGTACCCTGA---------------------------------------- : 660
LpMDHh7  : ACGCTTCCAGTCAATACCCTGATNTGAACCACGCCGCCNNAAANACTTCCAG-GGCGA---- : 693
LpMDHh8  : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 701
LpMDHh9  : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGCGGCGAGAAG : 701
LpMDHh10 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAANACT--------------- : 684
LpMDHh11 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 700
LpMDHh12 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 698
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGN------ : 692
LpMDHh15 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh16 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh17 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh18 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh19 : ACTCTTNCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh20 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh21 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh22 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 698
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : ACTCTTNCAGNC-ATACCCTGATGTGAACCACGCCACCGNGAAGACNTNCACTGCCNACAAG : 696
LpMDHh26 : ACTCTTCCAGTC-------------------------------------------------- : 646
LpMDHh27 : ACTCTTNCAGTCAATACCCTGATGTGAACCACGCCACCGTGAANACTTNCAGTGGCGAGAAG : 697
LpMDHh28 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh29 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh30 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 696
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGNGAAGACTTCCAGTGNCGAGANN : 696
LpMDHh34 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGG------- : 686
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGG------- : 685
LpMDHh43 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 693
LpMDHh44 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 692
LpMDHh45 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAA- : 690
LpMDHh46 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 692
LpMDHh47 : ACTNTTCCAGTCAGTNCCCTGATGTGAACCACNCCGCCGGAAANACTTCCAG---------- : 679
LpMDHh48 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGN--------- : 676
LpMDHh49 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 688
LpMDHh50 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAGGACTTCCAGTGGCGAGAAG : 666
LpMDHh51 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 649
LpMDHh52 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 615
LpMDHh53 : ACTCTTNCANNCNTTNCCCTGATGNNANCCNCGCCNCG------------------------ : 513
LpMDHh54 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 366
LpMDHh55 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 288
LpMDHh56 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 268
LpMDHh57 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 264
LpMDHh58 : ACTCTTCCAGTCAGTACCCTG-NGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG :  67
LpMDHh59 : -------------GTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG :  49
LpMDHh60 : -----------------------------------------------TTCNGTGGCAAG-AG :  14
LpMDHh61 : ------------------------------------------------------GCGAGAAG :   8
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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                  *       760         *       780         *       800
LpMDHh1  : CCTGTTCGCGAACTTGTTAAAGACGATG---------------------------------- : 770
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGNTCATTGCCACTGTCCA : 763
LpMDHh9  : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCANGGGTCATTGCCACTGTCCA : 763
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : CCTGTTC------------------------------------------------------- : 707
LpMDHh12 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh16 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh17 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 759
LpMDHh18 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh19 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh20 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 759
LpMDHh21 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTNAATGCAGGGTTCATTGCCACTGNCCA : 760
LpMDHh22 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : CCTGTTCGCGAACT------------------------------------------------ : 711
LpMDHh28 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh29 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh30 : CCTGTTCGCGAACTTGNTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 758
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 755
LpMDHh44 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 754
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : CCTGTTCG------------------------------------------------------ : 700
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 750
LpMDHh50 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 728
LpMDHh51 : CCTGTTCGCGAACTTGTTAAAGACGAT----------------------------------- : 676
LpMDHh52 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 677
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 428
LpMDHh55 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 350
LpMDHh56 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 330
LpMDHh57 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 326
LpMDHh58 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 129
LpMDHh59 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 111
LpMDHh60 : CCTGTTCGCG-ACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA :  75
LpMDHh61 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA :  70
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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                   *        820         *        840         *        860
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : GCAGCGTGGTGCTGCAATCATCAAAGCGAG-------------------------------- : 793
LpMDHh9  : GCAGCGTGGNGCTGCAATCATCAAAGNGAGGAAC---------------------------- : 797
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNCA--------------------- : 801
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : GCAG---------------------------------------------------------- : 764
LpMDHh16 : GCAGCGTGG----------------------------------------------------- : 769
LpMDHh17 : GCANCGTGGTG--------------------------------------------------- : 770
LpMDHh18 : GCAGCGTGGTGCTGCAATC------------------------------------------- : 779
LpMDHh19 : ACAGCGTGGTGCTGCAATCATCAAAGCG---------------------------------- : 788
LpMDHh20 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGC--------------------------- : 794
LpMDHh21 : GCAGCGTGGTGCTGCNATCATCAAAGCGAGGAAGCT[illegible]------------------------- : 797
LpMDHh22 : GCAGCGTGGNGCTGC-ATCATCAAAGCGAGGAAGCTCT[illegible]CAGT------------------- : 802
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : GCAGCGTGGTG--------------------------------------------------- : 768
LpMDHh29 : GCAGCGTGGTGCTGCAATCATCAAAG------------------------------------ : 783
LpMDHh30 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNCAGTGC----------------- : 803
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : GCAGCGTGGTGCTGCAATCAT[illegible]---------------------------------------- : 779
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : GCAGCGTG------------------------------------------------------ : 763
LpMDHh44 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT-------------------------- : 790
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT-------------------------- : 786
LpMDHh50 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTG------------------ : 772
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 739
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT[illegible]TCCAGTGCTCT[illegible]T[illegible]TGCTGCCAGCT : 490
LpMDHh55 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 412
LpMDHh56 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 392
LpMDHh57 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 388
LpMDHh58 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 191
LpMDHh59 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 173
LpMDHh60 : GCAGCGNGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 137
LpMDHh61 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 132
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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		* 880 * 900 * 920 *		
LpMDHh1	:	--	:	-
LpMDHh2	:	--	:	-
LpMDHh3	:	--	:	-
LpMDHh4	:	--	:	-
LpMDHh5	:	--	:	-
LpMDHh6	:	--	:	-
LpMDHh7	:	--	:	-
LpMDHh8	:	--	:	-
LpMDHh9	:	--	:	-
LpMDHh10	:	--	:	-
LpMDHh11	:	--	:	-
LpMDHh12	:	--	:	-
LpMDHh13	:	--	:	-
LpMDHh14	:	--	:	-
LpMDHh15	:	--	:	-
LpMDHh16	:	--	:	-
LpMDHh17	:	--	:	-
LpMDHh18	:	--	:	-
LpMDHh19	:	--	:	-
LpMDHh20	:	--	:	-
LpMDHh21	:	--	:	-
LpMDHh22	:	--	:	-
LpMDHh23	:	--	:	-
LpMDHh24	:	--	:	-
LpMDHh25	:	--	:	-
LpMDHh26	:	--	:	-
LpMDHh27	:	--	:	-
LpMDHh28	:	--	:	-
LpMDHh29	:	--	:	-
LpMDHh30	:	--	:	-
LpMDHh31	:	--	:	-
LpMDHh32	:	--	:	-
LpMDHh34	:	--	:	-
LpMDHh35	:	--	:	-
LpMDHh36	:	--	:	-
LpMDHh37	:	--	:	-
LpMDHh38	:	--	:	-
LpMDHh39	:	--	:	-
LpMDHh40	:	--	:	-
LpMDHh41	:	--	:	-
LpMDHh42	:	--	:	-
LpMDHh43	:	--	:	-
LpMDHh44	:	--	:	-
LpMDHh45	:	--	:	-
LpMDHh46	:	--	:	-
LpMDHh47	:	--	:	-
LpMDHh48	:	--	:	-
LpMDHh49	:	--	:	-
LpMDHh50	:	--	:	-
LpMDHh51	:	--	:	-
LpMDHh52	:	CTGCTTGTGACCACATCCGTGATT--------------------------------------	:	763
LpMDHh53	:	--	:	-
LpMDHh54	:	CTGCTTGTGACCACATCCGGGATTGGGTTCTCGGAACCCCTGANGGAACATTTGTTTCCATG	:	552
LpMDHh55	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTTGGAACCCCTGAGGGAACATTTGTTTCCATG	:	474
LpMDHh56	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	454
LpMDHh57	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	450
LpMDHh58	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	253
LpMDHh59	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	235
LpMDHh60	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	199
LpMDHh61	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG	:	194
LpMDHh62	:	--	:	-
LpMDHh63	:	--	:	-
LpMDHh64	:	--	:	-

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                          940         *         960         *         980         *
LpMDHh1  : -------------------------------------------------------------- :   -
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LpMDHh50 : -------------------------------------------------------------- :   -
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : GGTGTGTATTCTGATGGNT-ATACNGGGTGCCTGGTGGGCTTATCTACTCCTTNCCAGNAAC : 613
LpMDHh55 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 536
LpMDHh56 : GNTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 516
LpMDHh57 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 512
LpMDHh58 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 315
LpMDHh59 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 297
LpMDHh60 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 261
LpMDHh61 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 256
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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                  1000         *        1020         *        1040         *
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
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LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : TTGCTGNGGGGGGGAATGGACAATTGNTCAAAGGCTNCCNATCNACNAGTT----------- : 664
LpMDHh55  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 598
LpMDHh56  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 578
LpMDHh57  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 574
LpMDHh58  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 377
LpMDHh59  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGGTCGACGAGTTCTCAAGAAAGA : 359
LpMDHh60  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 323
LpMDHh61  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 318
LpMDHh62  : --------------------------------CCTTCCCGAAACCCGAGTTCTC-TTTTAG- :  28
LpMDHh63  : -------------------------------------------------------------- :   -
LpMDHh64  : -------------------------------------------------------------- :   -
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                1060         *         1080         *         1100         *
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
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LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 660
LpMDHh56 : AGATGGATGCCACAGCCCAGGAGCTCTCGNAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 640
LpMDHh57 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 636
LpMDHh58 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 439
LpMDHh59 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTTGCCTACTCGTGCCTCGAG : 421
LpMDHh60 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 385
LpMDHh61 : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 380
LpMDHh62 : AGA-GGACGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGTTNTCGCCTACTCGCGCCTCGAG :  89
LpMDHh63 : -----------------------CCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG :  38
LpMDHh64 : -------------------------------------------------------------- :   -
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               1120        *        1140        *        1160        *        11
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
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LpMDHh54  : -------------------------------------------------------------- :   -
LpMDHh55  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTN : 722
LpMDHh56  : TAACTGCATACCAGGGAGCAGCTGTCGCTCTGATGTTTTGAATAAAA-GNACATTTTGNCTN : 701
LpMDHh57  : TAACTGCATACCAGGGAGCAGCTGCCGCTCT------------------------------- : 667
LpMDHh58  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 501
LpMDHh59  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 483
LpMDHh60  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 447
LpMDHh61  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 442
LpMDHh62  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 151
LpMDHh63  : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 100
LpMDHh64  : -------------------------------------------------------------- :   -
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          80        *      1200         *      1220         *      1240
LpMDHh1  : -------------------------------------------------------------- :    -
LpMDHh2  : -------------------------------------------------------------- :    -
LpMDHh3  : -------------------------------------------------------------- :    -
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LpMDHh53 : -------------------------------------------------------------- :    -
LpMDHh54 : -------------------------------------------------------------- :    -
LpMDHh55 : CATGAAACTCAT-------------------------------------------------- :  734
LpMDHh56 : CATG---------------------------------------------------------- :  705
LpMDHh57 : -------------------------------------------------------------- :    -
LpMDHh58 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG :  563
LpMDHh59 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG :  545
LpMDHh60 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTGAGCTGGTTTTTCCAG :  509
LpMDHh61 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG :  504
LpMDHh62 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG :  213
LpMDHh63 : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG :  162
LpMDHh64 : -------------------------------------------------------------- :    -
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                     *     1260        *     1280        *     1300
LpMDHh1  : -------------------------------------------------------------- :   -
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LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 625
LpMDHh59 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 607
LpMDHh60 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 571
LpMDHh61 : TGTGTATGAATGAGGCTTTTGTAGCGCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 566
LpMDHh62 : TGTGTATGANTGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 275
LpMDHh63 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 224
LpMDHh64 : -------GNAAGNAGCTTTTGTAGCTCTATTTTCGCCTGNAGATTTACAGGACAGGATATTG :  55
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                     *        1320         *        1340         *        1360
LpMDHh1  : -------------------------------------------------------------- :  -
LpMDHh2  : -------------------------------------------------------------- :  -
LpMDHh3  : -------------------------------------------------------------- :  -
LpMDHh4  : -------------------------------------------------------------- :  -
LpMDHh5  : -------------------------------------------------------------- :  -
LpMDHh6  : -------------------------------------------------------------- :  -
LpMDHh7  : -------------------------------------------------------------- :  -
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LpMDHh9  : -------------------------------------------------------------- :  -
LpMDHh10 : -------------------------------------------------------------- :  -
LpMDHh11 : -------------------------------------------------------------- :  -
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LpMDHh41 : -------------------------------------------------------------- :  -
LpMDHh42 : -------------------------------------------------------------- :  -
LpMDHh43 : -------------------------------------------------------------- :  -
LpMDHh44 : -------------------------------------------------------------- :  -
LpMDHh45 : -------------------------------------------------------------- :  -
LpMDHh46 : -------------------------------------------------------------- :  -
LpMDHh47 : -------------------------------------------------------------- :  -
LpMDHh48 : -------------------------------------------------------------- :  -
LpMDHh49 : -------------------------------------------------------------- :  -
LpMDHh50 : -------------------------------------------------------------- :  -
LpMDHh51 : -------------------------------------------------------------- :  -
LpMDHh52 : -------------------------------------------------------------- :  -
LpMDHh53 : -------------------------------------------------------------- :  -
LpMDHh54 : -------------------------------------------------------------- :  -
LpMDHh55 : -------------------------------------------------------------- :  -
LpMDHh56 : -------------------------------------------------------------- :  -
LpMDHh57 : -------------------------------------------------------------- :  -
LpMDHh58 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCGGTGTGTA : 687
LpMDHh59 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCA----------------------- : 646
LpMDHh60 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA : 633
LpMDHh61 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTA------------ : 616
LpMDHh62 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA : 337
LpMDHh63 : GCAGGAAGATTGGAACAATTTGACGTCTGACAAAAAAAAAA--------------------- : 265
LpMDHh64 : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTA-TATTCCTGTGTGTA : 116
```

	* 1380 * 1400 * 1420		
LpMDHh1	--	:	-
LpMDHh2	--	:	-
LpMDHh3	--	:	-
LpMDHh4	--	:	-
LpMDHh5	--	:	-
LpMDHh6	--	:	-
LpMDHh7	--	:	-
LpMDHh8	--	:	-
LpMDHh9	--	:	-
LpMDHh10	--	:	-
LpMDHh11	--	:	-
LpMDHh12	--	:	-
LpMDHh13	--	:	-
LpMDHh14	--	:	-
LpMDHh15	--	:	-
LpMDHh16	--	:	-
LpMDHh17	--	:	-
LpMDHh18	--	:	-
LpMDHh19	--	:	-
LpMDHh20	--	:	-
LpMDHh21	--	:	-
LpMDHh22	--	:	-
LpMDHh23	--	:	-
LpMDHh24	--	:	-
LpMDHh25	--	:	-
LpMDHh26	--	:	-
LpMDHh27	--	:	-
LpMDHh28	--	:	-
LpMDHh29	--	:	-
LpMDHh30	--	:	-
LpMDHh31	--	:	-
LpMDHh32	--	:	-
LpMDHh34	--	:	-
LpMDHh35	--	:	-
LpMDHh36	--	:	-
LpMDHh37	--	:	-
LpMDHh38	--	:	-
LpMDHh39	--	:	-
LpMDHh40	--	:	-
LpMDHh41	--	:	-
LpMDHh42	--	:	-
LpMDHh43	--	:	-
LpMDHh44	--	:	-
LpMDHh45	--	:	-
LpMDHh46	--	:	-
LpMDHh47	--	:	-
LpMDHh48	--	:	-
LpMDHh49	--	:	-
LpMDHh50	--	:	-
LpMDHh51	--	:	-
LpMDHh52	--	:	-
LpMDHh53	--	:	-
LpMDHh54	--	:	-
LpMDHh55	--	:	-
LpMDHh56	--	:	-
LpMDHh57	--	:	-
LpMDHh58	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGG-	:	748
LpMDHh59	--	:	-
LpMDHh60	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGA	:	695
LpMDHh61	--	:	-
LpMDHh62	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACATGATATTGGCAGGA	:	399
LpMDHh63	--	:	-
LpMDHh64	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCACGATATTGGCAGGA	:	178

```
                  *        1440         *        1460         *        1480
LpMDHh1   : ------------------------------------------------------------ :   -
LpMDHh2   : ------------------------------------------------------------ :   -
LpMDHh3   : ------------------------------------------------------------ :   -
LpMDHh4   : ------------------------------------------------------------ :   -
LpMDHh5   : ------------------------------------------------------------ :   -
LpMDHh6   : ------------------------------------------------------------ :   -
LpMDHh7   : ------------------------------------------------------------ :   -
LpMDHh8   : ------------------------------------------------------------ :   -
LpMDHh9   : ------------------------------------------------------------ :   -
LpMDHh10  : ------------------------------------------------------------ :   -
LpMDHh11  : ------------------------------------------------------------ :   -
LpMDHh12  : ------------------------------------------------------------ :   -
LpMDHh13  : ------------------------------------------------------------ :   -
LpMDHh14  : ------------------------------------------------------------ :   -
LpMDHh15  : ------------------------------------------------------------ :   -
LpMDHh16  : ------------------------------------------------------------ :   -
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LpMDHh18  : ------------------------------------------------------------ :   -
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LpMDHh20  : ------------------------------------------------------------ :   -
LpMDHh21  : ------------------------------------------------------------ :   -
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LpMDHh23  : ------------------------------------------------------------ :   -
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LpMDHh27  : ------------------------------------------------------------ :   -
LpMDHh28  : ------------------------------------------------------------ :   -
LpMDHh29  : ------------------------------------------------------------ :   -
LpMDHh30  : ------------------------------------------------------------ :   -
LpMDHh31  : ------------------------------------------------------------ :   -
LpMDHh32  : ------------------------------------------------------------ :   -
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LpMDHh46  : ------------------------------------------------------------ :   -
LpMDHh47  : ------------------------------------------------------------ :   -
LpMDHh48  : ------------------------------------------------------------ :   -
LpMDHh49  : ------------------------------------------------------------ :   -
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LpMDHh54  : ------------------------------------------------------------ :   -
LpMDHh55  : ------------------------------------------------------------ :   -
LpMDHh56  : ------------------------------------------------------------ :   -
LpMDHh57  : ------------------------------------------------------------ :   -
LpMDHh58  : ------------------------------------------------------------ :   -
LpMDHh59  : ------------------------------------------------------------ :   -
LpMDHh60  : GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAA--- : 750
LpMDHh61  : ------------------------------------------------------------ :   -
LpMDHh62  : GGATTGGAACAANNANANN----------------------------------------- : 418
LpMDHh63  : ------------------------------------------------------------ :   -
LpMDHh64  : GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTATTCTAAAAAAAAAAA : 236
```

Figure 31 Nucleotide sequence of LpMDHi

```
                   *        20         *        40         *        60
LpMDHi : GTNCATAAAGCTGCCCAAAGCAATNCGTGNAATATTATCAGTAACCCTGTCAATTCTACC :  60

                   *        80         *       100         *       120
LpMDHi : GTACCAATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATNCTAAGAGATTGTTG : 120

                   *       140         *       160         *
LpMDHi : GGGGTTGACAACNGTTNGATGNNANTGACAGACCNTGCTCTTNGNNGNCGAGGTNCN : 177
```

Figure 32 Deduced amino acid sequence of LpMDHi

```
                      *        20         *         40         *
LpMDHi : XHKAAQSNXXNIISNPVNSTVPIAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58
```

Figure 33 Nucleotide sequence of LpMDHj

```
                     *        20         *        40         *        60
LpMDHj : ANAAAGGAGCCGACGCAGGGGCGCAGAATTCCATCTGCTNACTCTGCCACCACCCAAGTT :  60

                     *        80         *       100         *       120
LpMDHj : GGACATGGCGTCAGCTGTTACAATCAGTTCAGTCAGCGCGCAGGCCGCTTTGGTTTCAAA : 120

                     *       140         *       160         *       180
LpMDHj : ACCAAGGAACCATGGCAGCACGAGCTACAGTGGCCTAAAGGCATCATCGTCGTCGATCAG : 180

                     *       200         *       220         *       240
LpMDHj : CTTCGAATCAGGAACATCATTCCTGGGCAAGACCGCCTCCCTCCGGGCAACTGTTACCAC : 240

                     *       260         *       280         *       300
LpMDHj : AAGGGTTGTGCCAAAGGCGAAGTCTGGGTCGCAGATATCGCCTCAGGCATCTTACAAGGT : 300

                     *       320         *       340         *       360
LpMDHj : GGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAGATGTC : 360

                     *       380         *       400         *       420
LpMDHj : TCCTCTGGTCTCGGAGCTGCGCCTGTATGATATCGCGAATGTCAAGGGCGTCGCTGCAGA : 420

                     *       440         *       460         *       480
LpMDHj : TCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCAGAGCTAGC : 480

                     *       500         *       520         *       540
LpMDHj : AGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAGCCAGG : 540

                     *       560         *       580         *       600
LpMDHj : CATGACCCGTGATGACCTTTTTAACATNAATGCGGGAATCGNCAAGTCGCTTATTGAGGC : 600

                     *       620         *       640         *       660
LpMDHj : TGTTGCAGACAATTGCCCTGAGGGCCTTATTCATATCATCAACAACCCCGGTCAAACTCC : 660

LpMDHj : CCCT : 664
```

re 34   Deduced amino acid sequence of LpMDHj

```
                     *        20         *        40         *        60
LpMDHj : XRSRRRGAEFHLXTLPPPKLDMASAVTISSVSAQAALVSKPRNHGSTSYSGLKASSSSIS :  60

                     *        80         *       100         *       120
LpMDHj : FESGTSFLGKTASLRATVTTRVVPKAKSGSQISPQASYKVAVLGAAGGIGQPLGLLIKMS : 120

                     *       140         *       160         *       180
LpMDHj : PLVSELRLYDIANVKGVAADLSHCNTPAQVMDFTGPAELAECLKGVDVVVIPAGVPRKPG : 180

                     *       200         *       220
LpMDHj : MTRDDLFNXNAGIXKSLIEAVADNCPEGLIHIINNPGQTPP : 221
```

re 35 Consensus contig nucleotide sequence of LpMDHk

```
                  *        20         *        40         *        60
LpMDHk : TNTTTANCCCNCCAANTATCCAGNANCCACCTGGCCCTACACANAANAAAAACAAAAANN :   60

                  *        80         *       100         *       120
LpMDHk : AACCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  120

                  *       140         *       160         *       180
LpMDHk : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC :  180

                  *       200         *       220         *       240
LpMDHk : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG :  240

                  *       260         *       280         *       300
LpMDHk : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC :  300

                  *       320         *       340         *       360
LpMDHk : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC :  360

                  *       380         *       400         *       420
LpMDHk : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG :  420

                  *       440         *       460         *       480
LpMDHk : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT :  480

                  *       500         *       520         *       540
LpMDHk : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA :  540

                  *       560         *       580         *       600
LpMDHk : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG :  600

                  *       620         *       640         *       660
LpMDHk : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT :  660

                  *       680         *       700         *       720
LpMDHk : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC :  720

                  *       740         *       760         *       780
LpMDHk : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG :  780

                  *       800         *       820         *       840
LpMDHk : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG :  840

                  *       860         *       880         *       900
LpMDHk : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT :  900

                  *       920         *       940         *       960
LpMDHk : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG :  960
```

```
                 *      980         *      1000         *      1020
LpMDHk : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC : 1020

                 *     1040         *      1060         *      1080
LpMDHk : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA : 1080

                 *     1100         *      1120         *      1140
LpMDHk : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT : 1140

                 *     1160         *      1180         *      1200
LpMDHk : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 1200

                 *     1220         *      1240         *      1260
LpMDHk : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 1260


LpMDHk : AAG : 1263
```

ure 36 Deduced amino acid sequence of LpMDHk

```
                    *        20         *        40         *        60
LpMDHk : XLXXQXSXXHLALHXXKTKXNQXARGEPGRTQQFPSAHQPKLEMASAVTISSVSAQAALV :  60

                    *        80         *       100         *       120
LpMDHk : SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY : 120

                    *       140         *       160         *       180
LpMDHk : KVAVLGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKGVAADLSHCNTPSQVMDFTGPAE : 180

                    *       200         *       220         *       240
LpMDHk : LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN : 240

                    *       260         *       280         *       300
LpMDHk : STVPIAAEILKQKGVYNPKKLFGVSTLDVVRANTFVAQKKNLSLIDVDVPVVGGHAGITI : 300

                    *       320         *       340         *       360
LpMDHk : LPLLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA : 360

                    *       380         *       400         *       420
LpMDHk : MAGDPDVYECTYVQSELTELPFFASRVKLGKDXVESIISSDLEGVTEYEAKALXALKAEL : 420

LpMDHk : K : 421
```

Figure 37 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHk

```
                        *        20         *        40         *        60
LpMDHk1  : TNTTTANCCCNCCAANTATCCAGNANCCACCTGCCCCCAACCA-AN-AAAAANAAAAAGN : 58
LpMDHk2  : --------------------------------GNGCCCGCACGGAANAAAAANAAAAANN : 28
LpMDHk3  : --------------------------------GNCCCC-CAACCAAGAAAAAACAAAAGC : 27
LpMDHk4  : ---------------------------------GNCCGCCANCCAANAAAANNAAAAANN : 27
LpMDHk5  : ---------------------------------GCCCCGANNCCAACAAAAANAAAAANN : 27
LpMDHk6  : ----------------------------------GCCN-CAACCNAGAAAAAAGAAAAGG : 25
LpMDHk7  : -----------------------------------GTTTCNCAGAN-AAAAACCNAAANT : 24
LpMDHk8  : -----------------------------------GTTTCNCAGAN-AAAAACCNAAAGN : 24
LpMDHk9  : -----------------------------------GNNACACANANNAAAAACAAAAANN : 25
LpMDHk10 : -----------------------------------GTTACACANANNAAAAACAAAAANN : 25
LpMDHk11 : -----------------------------------CCT-CAACC-A-ANAAAAGAAAAGC : 22
LpMDHk12 : ------------------------------------TTTCCCANANAACNAAAANTTTAN : 24
LpMDHk13 : -------------------------------------TTCCCCAAAANGAAAANTTTTAG : 23
LpMDHk14 : --------------------------------------ACACANANNAAAAANAAAAANN : 22
LpMDHk15 : --------------------------------------ACACANANNAAAAANAAAAANN : 22
LpMDHk16 : --------------------------------------ACACANNN-AA-AANCAAAAAG : 20
LpMDHk17 : ---------------------------------------CANNNNA-AA-AACAAAAAGN : 19
LpMDHk18 : ---------------------------------------GTTCCAAGAAAANGAAAAAAG : 21
LpMDHk19 : ----------------------------------------GNACCAGAAAAAGAAAAAAG : 20
LpMDHk20 : ----------------------------------------GNACCAGAAAAAGAAAAAAG : 20
LpMDHk21 : ----------------------------------------GNACCAGAAAAAGAAAAAAG : 20
LpMDHk22 : ----------------------------------------GNACCAGAAAAAGAAAAAAG : 20
LpMDHk23 : -----------------------------------------CANANNAAAAANAAAAANN : 19
LpMDHk24 : -----------------------------------------CANANNAAAAANAAAAANN : 19
LpMDHk25 : -----------------------------------------CANANNAAAAACAAAAANN : 19
LpMDHk26 : -----------------------------------------CANANNAAAAACAAAAANN : 19
LpMDHk27 : -----------------------------------------GACCAGAAAAAGAAAAAAG : 19
LpMDHk28 : -----------------------------------------GTCCAGAAAAAGAAAAAAG : 19
LpMDHk29 : ------------------------------------------ANNA-AAAG-NAAAAAGN : 16
LpMDHk30 : ------------------------------------------ANANNAAAANCAAAAANN : 18
LpMDHk31 : -------------------------------------------AANNAAAANNAAAAANN : 17
LpMDHk32 : --------------------------------------------NNNAAAAANAAAAANN : 16
LpMDHk33 : --------------------------------------------ANNAAAANCAAAAANN : 16
LpMDHk34 : --------------------------------------------NAGAAAAACAAAAAAG : 16
LpMDHk35 : --------------------------------------------GAGAAAAAAGAAAAGC : 16
LpMDHk36 : ---------------------------------------------ANAAAANCAAAAANN : 15
LpMDHk37 : -----------------------------------------------NAACANNNAAA-- : 11
LpMDHk38 : -----------------------------------------------GNACAC-ANANN- : 11
LpMDHk39 : ------------------------------------------------AAAGCAAAAANN : 12
LpMDHk40 : ------------------------------------------------GNCAC-ANANN- : 10
LpMDHk41 : ------------------------------------------------GANGCCANANN- : 11
LpMDHk42 : ------------------------------------------------GACCAGAAAA-- : 10
LpMDHk43 : -------------------------------------------------AAANAAAAANN : 11
LpMDHk44 : -------------------------------------------------AANCCAAAAAN : 11
LpMDHk45 : -------------------------------------------------AAACAAAAAAN : 11
LpMDHk46 : --------------------------------------------------GACAANANN- : 9
LpMDHk47 : --------------------------------------------------AANNAAAAAN : 10
LpMDHk48 : ---------------------------------------------------GN-NNAAN- : 7
LpMDHk49 : ----------------------------------------------------C-ANANN- : 6
LpMDHk50 : ----------------------------------------------------GNACCAG- : 7
LpMDHk51 : -----------------------------------------------------CANNNN- : 6
LpMDHk52 : -----------------------------------------------------CANANN- : 6
LpMDHk53 : -----------------------------------------------------CACCAG- : 6
LpMDHk54 : ------------------------------------------------------ANANN- : 5
LpMDHk55 : --------------------------------------------------------CAG- : 3
LpMDHk56 : ------------------------------------------------------------ : -
LpMDHk57 : ------------------------------------------------------------ : -
LpMDHk58 : ------------------------------------------------------------ : -
LpMDHk59 : ------------------------------------------------------------ : -
LpMDHk60 : ------------------------------------------------------------ : -
LpMDHk61 : ------------------------------------------------------------ : -
LpMDHk62 : ------------------------------------------------------------ : -
LpMDHk63 : ------------------------------------------------------------ : -
LpMDHk64 : ------------------------------------------------------------ : -
LpMDHk65 : ------------------------------------------------------------ : -
LpMDHk66 : ------------------------------------------------------------ : -
```

```
                        *        80         *        100         *        120
LpMDHk1  : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 118
LpMDHk2  : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  85
LpMDHk3  : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC :  86
LpMDHk4  : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  84
LpMDHk5  : ANCCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  85
LpMDHk6  : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC :  84
LpMDHk7  : ATCCAGNA-GC-AGGGGCGANCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  82
LpMDHk8  : NNCCAGNACGC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  83
LpMDHk9  : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  83
LpMDHk10 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  82
LpMDHk11 : AGCGCAGNCGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC :  81
LpMDHk12 : NACCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  82
LpMDHk13 : NACCAGNA-GC-AGNGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  81
LpMDHk14 : ACCAGNAG-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk15 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCGTCTGCTCACCAACCC :  79
LpMDHk16 : NACCAGNAG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  79
LpMDHk17 : NNCCAGNNG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  78
LpMDHk18 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk19 : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk20 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk21 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk22 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  80
LpMDHk23 : ACCCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  77
LpMDHk24 : ACCCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  77
LpMDHk25 : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  77
LpMDHk26 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  79
LpMDHk27 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  78
LpMDHk28 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  79
LpMDHk29 : NCCC-GNGG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  74
LpMDHk30 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  78
LpMDHk31 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  76
LpMDHk32 : ANCCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  75
LpMDHk33 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  75
LpMDHk34 : AGCCAGAG-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  75
LpMDHk35 : AGCCAG-ACGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC :  74
LpMDHk36 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  74
LpMDHk37 : A---A-GAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  67
LpMDHk38 : AAAAN-CAAAAAAGGGGCGAGCCGGGGCGCACACAGCAATTCCCATCTGCCCACCAACCC :  70
LpMDHk39 : ACCCAGNAGGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  72
LpMDHk40 : AAAAA-GAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  69
LpMDHk41 : AAAAANAAAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  70
LpMDHk42 : A---N-GAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  66
LpMDHk43 : ACCCAG-NNGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  70
LpMDHk44 : NACCAGNACGCAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  71
LpMDHk45 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  70
LpMDHk46 : AAAAATNANAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  68
LpMDHk47 : NACCAGNACGCAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  70
LpMDHk48 : AAAAA-NAAAANANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  66
LpMDHk49 : AAAAA-GAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  65
LpMDHk50 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  67
LpMDHk51 : AAAANCAAAAAAGGGNACGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  66
LpMDHk52 : AAAAANANAAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  65
LpMDHk53 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  66
LpMDHk54 : AAAAANAAAAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  64
LpMDHk55 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  63
LpMDHk56 : --AAA-AAAANAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  57
LpMDHk57 : ---AANNAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCCACCAACCC :  57
LpMDHk58 : ----------CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC :  50
LpMDHk59 : ----------ANAGGGGCNNGCCGGGGCGC-CGC-G-AATT-CCATCTG-CCNCC-A-CC :  43
LpMDHk60 : -----------------GGAGCCGGGGCNC-CGCAGCAATTCCCATCTGCTCACCAACCC :  42
LpMDHk61 : ----------------------GGGGGCGCACGCA-CAATTCCCATCTGCTCACCAACCC :  37
LpMDHk62 : ----------------------------NCA-GCAGCAATTCCCTNCTGCCCACCAACCC :  31
LpMDHk63 : -----------------------------GNCACNACATTGCCCNNCTGCCCACCAACCC :  31
LpMDHk64 : ---------------------------------------------TCTGCCCACCAACCC :  15
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
```

```
                           *        140          *         160          *         180
LpMDHk1   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 178
LpMDHk2   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 145
LpMDHk3   : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTCTGGTT : 146
LpMDHk4   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 144
LpMDHk5   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 145
LpMDHk6   : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTCTGGTT : 144
LpMDHk7   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk8   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 143
LpMDHk9   : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 143
LpMDHk10  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk11  : AAGTTGGNCATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTCTGGTT : 141
LpMDHk12  : AAGTTGGGCATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk13  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 141
LpMDHk14  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGTTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk15  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk16  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk17  : AAGTTGGGNATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk18  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCCTTGGTC : 140
LpMDHk19  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk20  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk21  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk22  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCCTTGGTC : 140
LpMDHk23  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk24  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk25  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk26  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGATC : 139
LpMDHk27  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk28  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk29  : AAGTTGGGGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 134
LpMDHk30  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk31  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 136
LpMDHk32  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk33  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAATCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk34  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk35  : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTCTGGTT : 134
LpMDHk36  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 134
LpMDHk37  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 127
LpMDHk38  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 130
LpMDHk39  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 132
LpMDHk40  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 129
LpMDHk41  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 130
LpMDHk42  : AAGTTGGACATGGCATCAGCTGNCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk43  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk44  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 131
LpMDHk45  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk46  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 128
LpMDHk47  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk48  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk49  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 125
LpMDHk50  : AAGTTGGACATGGCATCTGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 127
LpMDHk51  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk52  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 125
LpMDHk53  : AAGTTGGACATGGCATCAGCCGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk54  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 124
LpMDHk55  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 123
LpMDHk56  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 117
LpMDHk57  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 117
LpMDHk58  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 110
LpMDHk59  : AAGTTGGACATGGCATCAGCTGT-ACCATCAGTT-AGT-AGCGCCCAGGCCGCTCTGGTG : 100
LpMDHk60  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 102
LpMDHk61  : A--TTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC :  95
LpMDHk62  : A-NTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  90
LpMDHk63  : -ANTTGGA-ATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  89
LpMDHk64  : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  75
LpMDHk65  : ------------------------------------------------------------ :   -
LpMDHk66  : ------------------------------------------------------------ :   -
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                        *         200         *         220         *         240
LpMDHk1  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 238
LpMDHk2  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 205
LpMDHk3  : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 206
LpMDHk4  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 204
LpMDHk5  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 205
LpMDHk6  : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 204
LpMDHk7  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk8  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 203
LpMDHk9  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 203
LpMDHk10 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk11 : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 201
LpMDHk12 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk13 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 201
LpMDHk14 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk15 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk16 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk17 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 198
LpMDHk18 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk19 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk20 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk21 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk22 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk23 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCAGCATCATCGTCG : 197
LpMDHk24 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 197
LpMDHk25 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 197
LpMDHk26 : TCGAAACCAAGGAATCGTGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk27 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 198
LpMDHk28 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk29 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 194
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LpMDHk32 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195
LpMDHk33 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195
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LpMDHk36 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 194
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LpMDHk38 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 190
LpMDHk39 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 192
LpMDHk40 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 189
LpMDHk41 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 190
LpMDHk42 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk43 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk44 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 191
LpMDHk45 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk46 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 188
LpMDHk47 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk48 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk49 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 185
LpMDHk50 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 187
LpMDHk51 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk52 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 185
LpMDHk53 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk54 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 184
LpMDHk55 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 183
LpMDHk56 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 177
LpMDHk57 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 177
LpMDHk58 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 170
LpMDHk59 : T-AAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 159
LpMDHk60 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 162
LpMDHk61 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 155
LpMDHk62 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 150
LpMDHk63 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 149
LpMDHk64 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 135
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
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	* 260 * 280 * 300	
LpMDHk1 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCACCTCTCTTCGGGCGACTATC	: 298
LpMDHk2 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 265
LpMDHk3 :	ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT	: 266
LpMDHk4 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 264
LpMDHk5 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 265
LpMDHk6 :	ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT	: 264
LpMDHk7 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 262
LpMDHk8 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 263
LpMDHk9 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 263
LpMDHk10 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 262
LpMDHk11 :	ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGNCTCGCTGCGGGCGACTGTT	: 261
LpMDHk12 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 262
LpMDHk13 :	ATCAGCTTCGAATCANGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 261
LpMDHk14 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk15 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 259
LpMDHk16 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 259
LpMDHk17 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 258
LpMDHk18 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk19 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk20 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk21 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk22 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 260
LpMDHk23 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 257
LpMDHk24 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 257
LpMDHk25 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 257
LpMDHk26 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 259
LpMDHk27 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 258
LpMDHk28 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 259
LpMDHk29 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 254
LpMDHk30 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 258
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LpMDHk33 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 255
LpMDHk34 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 255
LpMDHk35 :	ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT	: 254
LpMDHk36 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 254
LpMDHk37 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 247
LpMDHk38 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 250
LpMDHk39 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 252
LpMDHk40 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 249
LpMDHk41 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 250
LpMDHk42 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 246
LpMDHk43 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 250
LpMDHk44 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 251
LpMDHk45 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 250
LpMDHk46 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 248
LpMDHk47 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 250
LpMDHk48 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 246
LpMDHk49 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 245
LpMDHk50 :	ATCAGCTTCGAATCTGGAGCATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 247
LpMDHk51 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 246
LpMDHk52 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGCC	: 245
LpMDHk53 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 246
LpMDHk54 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 244
LpMDHk55 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 243
LpMDHk56 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 237
LpMDHk57 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	:.237
LpMDHk58 :	ATCAGCTTCGAATCAGGGGCATCATTCCTGGACAAGACCGNCTCTCTTCGGGCGACTATC	: 230
LpMDHk59 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 219
LpMDHk60 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 222
LpMDHk61 :	ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC	: 215
LpMDHk62 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 210
LpMDHk63 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 209
LpMDHk64 :	ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC	: 195
LpMDHk65 :	--	: -
LpMDHk66 :	--	: -

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                   *        320         *        340         *        360
LpMDHk1  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 358
LpMDHk2  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 325
LpMDHk3  : ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 326
LpMDHk4  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 324
LpMDHk5  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 325
LpMDHk6  : ACCCCAAGGATTGNGCCAAAGGCAAAGTCTGGGTCTCANATATCGCCTCAGGCATCTTAC : 324
LpMDHk7  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 322
LpMDHk8  : ACCTCAAGGATTGTGCCAAAGGCAAAGGCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 323
LpMDHk9  : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 323
LpMDHk10 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 322
LpMDHk11 : ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 321
LpMDHk12 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 322
LpMDHk13 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 321
LpMDHk14 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk15 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319
LpMDHk16 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319
LpMDHk17 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 318
LpMDHk18 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk19 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk20 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk21 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk22 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 320
LpMDHk23 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 317
LpMDHk24 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 317
LpMDHk25 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 317
LpMDHk26 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319
LpMDHk27 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 318
LpMDHk28 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319
LpMDHk29 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 314
LpMDHk30 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 318
LpMDHk31 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 316
LpMDHk32 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 315
LpMDHk33 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 315
LpMDHk34 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 315
LpMDHk35 : ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 314
LpMDHk36 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 314
LpMDHk37 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 307
LpMDHk38 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 310
LpMDHk39 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 312
LpMDHk40 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 309
LpMDHk41 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 310
LpMDHk42 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 306
LpMDHk43 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 310
LpMDHk44 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 311
LpMDHk45 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 310
LpMDHk46 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 308
LpMDHk47 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 310
LpMDHk48 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 306
LpMDHk49 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 305
LpMDHk50 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTCAC : 307
LpMDHk51 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 306
LpMDHk52 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 305
LpMDHk53 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 306
LpMDHk54 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 304
LpMDHk55 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 303
LpMDHk56 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 297
LpMDHk57 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 297
LpMDHk58 : ACCTCAAGGATTGTGCCAAAGGCAAAGNCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 290
LpMDHk59 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 279
LpMDHk60 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 282
LpMDHk61 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCGCAGGCCTCGTAC : 275
LpMDHk62 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 270
LpMDHk63 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 269
LpMDHk64 : ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC : 255
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
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                   *      380         *        400         *      420
LpMDHk1  : AAGGTGGCGGTGCTTGGTGCTGACGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 418
LpMDHk2  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 385
LpMDHk3  : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGCCAACCACTGGGCCTGCTGATCAAG : 386
LpMDHk4  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 384
LpMDHk5  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 385
LpMDHk6  : AAGGNGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAN : 384
LpMDHk7  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 382
LpMDHk8  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383
LpMDHk9  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383
LpMDHk10 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 382
LpMDHk11 : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 381
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LpMDHk14 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
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LpMDHk18 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
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LpMDHk24 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 377
LpMDHk25 : AAGGTGGCGGTGTTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 377
LpMDHk26 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379
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LpMDHk60 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 342
LpMDHk61 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 335
LpMDHk62 : AAGGTGGCGGNGCTTGGTGCTGNCGGNGGCATNGGGCAACCACTGGGCCTGCTGATNAAG : 330
LpMDHk63 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 329
LpMDHk64 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 315
LpMDHk65 : -------------TTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG :  47
LpMDHk66 : ------------------------------------------------------------ :  -
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                        *       440         *        460         *       480
LpMDHk1  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGACAATGTCAAGGGAGTCGCT : 478
LpMDHk2  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 445
LpMDHk3  : ATGTCTCCTCTAGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 446
LpMDHk4  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 444
LpMDHk5  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 445
LpMDHk6  : ATGTCTCCTCTGGTCTCAN------------------------------------------ : 403
LpMDHk7  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk8  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 443
LpMDHk9  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 443
LpMDHk10 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk11 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 441
LpMDHk12 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk13 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 441
LpMDHk14 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk15 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
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LpMDHk17 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 438
LpMDHk18 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk19 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk20 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk21 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk22 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
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LpMDHk24 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 437
LpMDHk25 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 437
LpMDHk26 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
LpMDHk27 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 438
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LpMDHk32 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk33 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk34 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk35 : ATGTCTCCTCTGGTCTCANAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 434
LpMDHk36 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 434
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LpMDHk38 : ATGTCGCCTCTGGCCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 430
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LpMDHk40 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 429
LpMDHk41 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 430
LpMDHk42 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 426
LpMDHk43 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
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LpMDHk45 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
LpMDHk46 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 428
LpMDHk47 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
LpMDHk48 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk49 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 425
LpMDHk50 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 427
LpMDHk51 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk52 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 425
LpMDHk53 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk54 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 424
LpMDHk55 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 423
LpMDHk56 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 417
LpMDHk57 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCGGTATGATAATGCGAATGTCAAGGGCGTCGCT : 417
LpMDHk58 : ATGNNTCCTCTGGTCTCANAGCTGCGCCTGTATGATATTGCCAATGNCAAGGGAGTCGCT : 410
LpMDHk59 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 399
LpMDHk60 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 402
LpMDHk61 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 395
LpMDHk62 : ATG--------------------------------------------------------- : 333
LpMDHk63 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 389
LpMDHk64 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 375
LpMDHk65 : ATGTCTCCTCTCGTCTCGGAGCTGCGCCTGTATGATATCGCCAATGTCAAGGGAGTCGCT : 107
LpMDHk66 : ------------------------------------------------------------ : -
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                  .    *      500          *         520          *        540
LpMDHk1  : GCAGATCTCAGNCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 538
LpMDHk2  : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 505
LpMDHk3  : GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 506
LpMDHk4  : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 504
LpMDHk5  : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 505
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : GCAGATCTCAGCCACTGGAACACGCCTTCTCAGGTCATGGACTTGACTGGCCCAGCAGAA : 502
LpMDHk8  : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 503
LpMDHk9  : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 503
LpMDHk10 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 502
LpMDHk11 : GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 501
LpMDHk12 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 502
LpMDHk13 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 501
LpMDHk14 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 500
LpMDHk15 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 499
LpMDHk16 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 499
LpMDHk17 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 498
LpMDHk18 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 500
LpMDHk19 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCTGAA : 500
LpMDHk20 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 500
LpMDHk21 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 500
LpMDHk22 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 500
LpMDHk23 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 497
LpMDHk24 : GCAGATCTCAGCCGCTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 497
LpMDHk25 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 497
LpMDHk26 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 499
LpMDHk27 : GCAGGTCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGTCCAGCAGAA : 498
LpMDHk28 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 499
LpMDHk29 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCGCTGGCCCAGCAGAA : 494
LpMDHk30 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 498
LpMDHk31 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 496
LpMDHk32 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 495
LpMDHk33 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 495
LpMDHk34 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 495
LpMDHk35 : GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 494
LpMDHk36 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 494
LpMDHk37 : GCCGATCTCAGCCACCGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 487
LpMDHk38 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 490
LpMDHk39 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 492
LpMDHk40 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 489
LpMDHk41 : GCCGATCTCAGCCACTGCAACACGCCTGCTCTGGTCATGGACTTCACTGGCCCCGCGGAA : 490
LpMDHk42 : GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 486
LpMDHk43 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 490
LpMDHk44 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 491
LpMDHk45 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGGCTTCACTGGCCCAGCAGAA : 490
LpMDHk46 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 488
LpMDHk47 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 490
LpMDHk48 : GCCGACCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 486
LpMDHk49 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 485
LpMDHk50 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 487
LpMDHk51 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 486
LpMDHk52 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 485
LpMDHk53 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 486
LpMDHk54 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 484
LpMDHk55 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 483
LpMDHk56 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 477
LpMDHk57 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 477
LpMDHk58 : GCAAATCTCANNCACTGCAACACGCCTTCTNAGGNCATGGACTTCACTGGNCCANCANAA : 470
LpMDHk59 : GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 459
LpMDHk60 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 462
LpMDHk61 : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 455
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 449
LpMDHk64 : GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA : 435
LpMDHk65 : GCAGATCTCAGCCACTGCAACACGCCTGCTCAGGCCATGGACTTCACTGGCCCCGCGGAA : 167
LpMDHk66 : -----GATCAGCC:CTGCAACACGCCTGCTCAGGCCATGGACTTCACTGGCCCCGCGGAA :  54
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                         *        560         *        580         *        600
LpMDHk1  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGNCATCCCTGCGGGTGTNCCAAGGAAG : 598
LpMDHk2  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 565
LpMDHk3  : CTAGCGGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 566
LpMDHk4  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCTCAAGGAAG : 564
LpMDHk5  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 565
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : CTAGCTGACTGCTTGAAAGGTGCTGATGTTGNCNGCATCCCTGCGGNNGTCNCAAGGAA- : 561
LpMDHk8  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 563
LpMDHk9  : CTAGCTGGCTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 563
LpMDHk10 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 562
LpMDHk11 : CTAGCGGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 561
LpMDHk12 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 562
LpMDHk13 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCTCAAGGAAG : 561
LpMDHk14 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk15 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk16 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk17 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk18 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk19 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk20 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk21 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk22 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk23 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk24 : CTAGCTGACTGCTTGAGAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk25 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk26 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk27 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk28 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk29 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTNCCAAGGAAG : 554
LpMDHk30 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk31 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 556
LpMDHk32 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk33 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk34 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk35 : CTAGCGGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 554
LpMDHk36 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 554
LpMDHk37 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTNCCAAGGAAG : 547
LpMDHk38 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCG-NATCCCTGCGGGTGTTCCAAGGAAG : 549
LpMDHk39 : CTAGCTGACTGCTTGAAAGG-GTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 551
LpMDHk40 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 549
LpMDHk41 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAN : 550
LpMDHk42 : CTAGCGGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk43 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk44 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 551
LpMDHk45 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk46 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 548
LpMDHk47 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk48 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk49 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 545
LpMDHk50 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 547
LpMDHk51 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk52 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 545
LpMDHk53 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk54 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 544
LpMDHk55 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 543
LpMDHk56 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 537
LpMDHk57 : CTAGCAGAGTGCTTGAAAGGCGTGGATGCTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 537
LpMDHk58 : CTA--------------------------------------------------------- : 473
LpMDHk59 : CTAGCGGACTGCTTGAAANGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 519
LpMDHk60 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 522
LpMDHk61 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 515
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 509
LpMDHk64 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGNCGTCATCCCTGCGGGTGTCCCAAGGAAG : 495
LpMDHk65 : CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 227
LpMDHk66 : CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 114
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                  *        620         *        640         *        660
[illegible]DHk1 : CCAGNCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNNAAGTCGCTTATT : 658
LpMDHk2  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 625
LpMDHk3  : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 626
LpMDHk4  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 624
LpMDHk5  : CCAGGCACGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 625
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 623
LpMDHk9  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 623
LpMDHk10 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 622
LpMDHk11 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 621
LpMDHk12 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 622
LpMDHk13 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 621
LpMDHk14 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk15 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk16 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk17 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk18 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk19 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNCAAGTCGCTTATT : 620
LpMDHk20 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk21 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk22 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk23 : CCAGGCATGACCCATGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk24 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk25 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk26 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk27 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk28 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk29 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 614
LpMDHk30 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk31 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 616
LpMDHk32 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk33 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk34 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk35 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 614
LpMDHk36 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 614
LpMDHk37 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGG-CATCGTC-AGNNGCTTATC : 605
LpMDHk38 : CCAGGCATGACCCGTGATGACCTTTNTAACATCAATGCGGGCATCGNCAAGNCGCTTATC : 609
LpMDHk39 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 611
LpMDHk40 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 609
LpMDHk41 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 610
LpMDHk42 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk43 : CCAGACAACTGCCGTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAACTCCACTGTC : 610
LpMDHk44 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 611
LpMDHk45 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 610
LpMDHk46 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 608
LpMDHk47 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 610
LpMDHk48 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk49 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 605
LpMDHk50 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 607
LpMDHk51 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk52 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 605
LpMDHk53 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk54 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 604
LpMDHk55 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 603
LpMDHk56 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 597
LpMDHk57 : CCAGGCATGACCCGTGATGACCTTTTTAACATCNATGCGGGCATCGTCAAGTCGCTTATC : 597
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGCCAAGTCGCTTATC : 579
LpMDHk60 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 582
LpMDHk61 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 575
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 569
LpMDHk64 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 555
LpMDHk65 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 287
LpMDHk66 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 174
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                        *        680         *        700         *        720
LpMDHk1  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCANCNACCC------- : 711
LpMDHk2  : GAGGCTGTTGCAGACAACTGCC-------------------------------------- : 647
LpMDHk3  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 686
LpMDHk4  : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 684
LpMDHk5  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 685
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATC------------------------ : 659
LpMDHk9  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 683
LpMDHk10 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 682
LpMDHk11 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 681
LpMDHk12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCAAC : 682
LpMDHk13 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 681
LpMDHk14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCACN : 680
LpMDHk15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk16 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk17 : GAGGCTGTTGCAGACA-------------------------------------------- : 634
LpMDHk18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk19 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGNCAAC : 680
LpMDHk20 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk21 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk22 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk23 : GAGGCTGTTGC------------------------------------------------- : 628
LpMDHk24 : GAGGCTGTTGCAGACAACTGCCC------------------------------------- : 640
LpMDHk25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 677
LpMDHk26 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 678
LpMDHk28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 678
LpMDHk31 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 676
LpMDHk32 : GAGGCTGTTGCAGACAACTGCC-------------------------------------- : 637
LpMDHk33 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 675
LpMDHk34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 675
LpMDHk35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk37 : GAGGCTGTTGCAGAC-ACT-GCCTGAGGCCTT-ATCCATATTATCA-NNACCCGG--GAC : 659
LpMDHk38 : GAGGCTGTTGCAGACAACTGCCCTGAGGNCTTCATCCATATTATGAGAACCCCGGNCAAC : 669
LpMDHk39 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTT--------------------------- : 644
LpMDHk40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 669
LpMDHk41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 670
LpMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 666
LpMDHk43 : GCGATTGGTGCTGAGATCTAAACAGAA--------------------------------- : 637
LpMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 671
LpMDHk45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 670
LpMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCAT--------------------- : 647
LpMDHk47 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAAC--------- : 661
LpMDHk48 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCA-------------------------- : 640
LpMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 665
LpMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 667
LpMDHk51 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCNA- : 665
LpMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 665
LpMDHk53 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 666
LpMDHk54 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 664
LpMDHk55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 663
LpMDHk56 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 657
LpMDHk57 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCNAC : 657
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : AAGGCTGTTGCAGACAACTGCCTTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 639
LpMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 642
LpMDHk61 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 635
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 629
LpMDHk64 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 615
LpMDHk65 : GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 347
LpMDHk66 : GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 234
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                *        740         *         760         *         780
LpMDHk1  : -------------------------------------------------------------- :   -
LpMDHk2  : -------------------------------------------------------------- :   -
LpMDHk3  : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 746
LpMDHk4  : TNCACTGT------------------------------------------------------ : 692
LpMDHk5  : TNCACTGTGA---------------------------------------------------- : 695
LpMDHk6  : -------------------------------------------------------------- :   -
LpMDHk7  : -------------------------------------------------------------- :   -
LpMDHk8  : -------------------------------------------------------------- :   -
LpMDHk9  : TNCACTGTGCCGATTGCTGCTGA--------------------------------------- : 706
LpMDHk10 : TCCACTGTGCCGATTGCTGCTGAA-------------------------------------- : 706
LpMDHk11 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCCAAGAAG : 741
LpMDHk12 : TNCACTGTG----------------------------------------------------- : 691
LpMDHk13 : TNCACTGTGCCGATTGCTGCTGAG-------------------------------------- : 705
LpMDHk14 : -------------------------------------------------------------- :   -
LpMDHk15 : TCCACTGTGCCGATTGCTGCTGAGAT------------------------------------ : 705
LpMDHk16 : TNCACTGTGCCGATTGCTGCTGAGATA----------------------------------- : 706
LpMDHk17 : -------------------------------------------------------------- :   -
LpMDHk18 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk19 : TCCACTGNGCCGATTGCTGCTGANATTCTGAAACANAAGGGCGNNTACAACCCCAANAAG : 740
LpMDHk20 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk21 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk22 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk23 : -------------------------------------------------------------- :   -
LpMDHk24 : -------------------------------------------------------------- :   -
LpMDHk25 : TCCACTGTGCCGATTGCTGCT----------------------------------------- : 698
LpMDHk26 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAAAN---------------------------- : 713
LpMDHk27 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 738
LpMDHk28 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 739
LpMDHk29 : TGCACTGTGC---------------------------------------------------- : 684
LpMDHk30 : TNCACTGTGCCGATTGN--------------------------------------------- : 695
LpMDHk31 : TNCACTGTGCCGATTGCTG------------------------------------------- : 695
LpMDHk32 : -------------------------------------------------------------- :   -
LpMDHk33 : -------------------------------------------------------------- :   -
LpMDHk34 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNT-CGACCCCAAGAAG : 734
LpMDHk35 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 734
LpMDHk36 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAA------------------------------ : 706
LpMDHk37 : TGCACGGTGCCGATTGCTGNAAT--------------------------------------- : 682
LpMDHk38 : TCCACGGGGCCGATTGNTGCAGAGATTCTGAAACAGAA-GGCGT------------------ : 712
LpMDHk39 : -------------------------------------------------------------- :   -
LpMDHk40 : TNCACGGTGCCGAT------------------------------------------------ : 683
LpMDHk41 : TCCACGGTGCCGATTGCTGCAGAGA------------------------------------- : 695
LpMDHk42 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 726
LpMDHk43 : -------------------------------------------------------------- :   -
LpMDHk44 : TNCACTGTGCCGATT----------------------------------------------- : 686
LpMDHk45 : TNCACTGTGCCGATTGCTGCTGG--------------------------------------- : 693
LpMDHk46 : -------------------------------------------------------------- :   -
LpMDHk47 : -------------------------------------------------------------- :   -
LpMDHk48 : -------------------------------------------------------------- :   -
LpMDHk49 : TCCACGGTGCCGATTG---------------------------------------------- : 681
LpMDHk50 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 727
LpMDHk51 : -------------------------------------------------------------- :   -
LpMDHk52 : TNCACGGTGCCGATN----------------------------------------------- : 680
LpMDHk53 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 726
LpMDHk54 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAG------------------------ : 702
LpMDHk55 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 723
LpMDHk56 : TNCACGGTGCCGATTGCTGCAGAGATTCTGAAACA-AAAGGCGTCTACAAC---------- : 707
LpMDHk57 : TCCACGGNGCCGATTGNTGCA-ANATTTTGG------------------------------- : 687
LpMDHk58 : -------------------------------------------------------------- :   -
LpMDHk59 : TNC----------------------------------------------------------- : 642
LpMDHk60 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 702
LpMDHk61 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAGCCCCAAGAAG : 695
LpMDHk62 : -------------------------------------------------------------- :   -
LpMDHk63 : T------------------------------------------------------------- : 630
LpMDHk64 : TNCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAA---- : 671
LpMDHk65 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGTGTCTACAACCCCAAGAAG : 407
LpMDHk66 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGTGTCTACAACCCCAAGAAG : 294
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                 *       800         *       820         *       840
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : CTCTTCGGGGTTTNCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANA----- : 801
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAANAAN : 801
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : CTCTTCGGGGTTTCCACC------------------------------------------ : 758
LpMDHk19 : CTCTTNGGGGNTTNCACCCTG--------------------------------------- : 761
LpMDHk20 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAA---------------------------- : 772
LpMDHk21 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAN---------------------------- : 772
LpMDHk22 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAAGAAG : 800
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGA--------------------------- : 771
LpMDHk28 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAG-------------------------- : 773
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : CTTTTCNGGGNTTACACCCTGGATGTTGCC------------------------------ : 764
LpMDHk35 : CTCTTCGGGGNTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCT--------- : 785
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : CTCTTCGGGGTTTNCACCCTGGATGTTGTCAGAGCTAACACATTTGNAGCTCANAANAAG : 786
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : CTCTTCGGGGTTTC---------------------------------------------- : 741
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGGGCTAACACATT---------------- : 770
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : CTCTTCGGGGTTTCCGCCCTGGATGTTGTCAGGGCTAACACATTTGTAGCTCAA------ : 777
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 762
LpMDHk61 : CTCTTA------------------------------------------------------ : 701
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 467
LpMDHk66 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 354
```

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                         *       860         *       880         *       900
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : A----------------------------------------------------------- : 802
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : AACCTCA----------------------------------------------------- : 807
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : AACCTCAGTCTTATCG-------------------------------------------- : 802
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : AACCT------------------------------------------------------- : 767
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT : 527
LpMDHk66 : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT : 414
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                    *       920         *       940         *       960
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
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LpMDHk22 : ------------------------------------------------------------ :   -
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LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
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LpMDHk28 : ------------------------------------------------------------ :   -
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LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
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LpMDHk34 : ------------------------------------------------------------ :   -
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LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
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LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
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LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
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LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG : 587
LpMDHk66 : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG : 474
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```
                   *        980         *        1000          *        1020
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
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LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
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LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : CTGACAAAGAGGATACAGAACGCTGGGACAGAGG[illegible]GGTGGAGGCGAA------------- : 634
LpMDHk66 : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC : 534
```

```
                  *        1040         *        1060         *        1080
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA : 594
```

```
                   *      1100         *      1120         *      1140
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
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LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT : 654
```

```
                         *        1160         *        1180         *        1200
LpMDHk1   : ------------------------------------------------------------ :  -
LpMDHk2   : ------------------------------------------------------------ :  -
LpMDHk3   : ------------------------------------------------------------ :  -
LpMDHk4   : ------------------------------------------------------------ :  -
LpMDHk5   : ------------------------------------------------------------ :  -
LpMDHk6   : ------------------------------------------------------------ :  -
LpMDHk7   : ------------------------------------------------------------ :  -
LpMDHk8   : ------------------------------------------------------------ :  -
LpMDHk9   : ------------------------------------------------------------ :  -
LpMDHk10  : ------------------------------------------------------------ :  -
LpMDHk11  : ------------------------------------------------------------ :  -
LpMDHk12  : ------------------------------------------------------------ :  -
LpMDHk13  : ------------------------------------------------------------ :  -
LpMDHk14  : ------------------------------------------------------------ :  -
LpMDHk15  : ------------------------------------------------------------ :  -
LpMDHk16  : ------------------------------------------------------------ :  -
LpMDHk17  : ------------------------------------------------------------ :  -
LpMDHk18  : ------------------------------------------------------------ :  -
LpMDHk19  : ------------------------------------------------------------ :  -
LpMDHk20  : ------------------------------------------------------------ :  -
LpMDHk21  : ------------------------------------------------------------ :  -
LpMDHk22  : ------------------------------------------------------------ :  -
LpMDHk23  : ------------------------------------------------------------ :  -
LpMDHk24  : ------------------------------------------------------------ :  -
LpMDHk25  : ------------------------------------------------------------ :  -
LpMDHk26  : ------------------------------------------------------------ :  -
LpMDHk27  : ------------------------------------------------------------ :  -
LpMDHk28  : ------------------------------------------------------------ :  -
LpMDHk29  : ------------------------------------------------------------ :  -
LpMDHk30  : ------------------------------------------------------------ :  -
LpMDHk31  : ------------------------------------------------------------ :  -
LpMDHk32  : ------------------------------------------------------------ :  -
LpMDHk33  : ------------------------------------------------------------ :  -
LpMDHk34  : ------------------------------------------------------------ :  -
LpMDHk35  : ------------------------------------------------------------ :  -
LpMDHk36  : ------------------------------------------------------------ :  -
LpMDHk37  : ------------------------------------------------------------ :  -
LpMDHk38  : ------------------------------------------------------------ :  -
LpMDHk39  : ------------------------------------------------------------ :  -
LpMDHk40  : ------------------------------------------------------------ :  -
LpMDHk41  : ------------------------------------------------------------ :  -
LpMDHk42  : ------------------------------------------------------------ :  -
LpMDHk43  : ------------------------------------------------------------ :  -
LpMDHk44  : ------------------------------------------------------------ :  -
LpMDHk45  : ------------------------------------------------------------ :  -
LpMDHk46  : ------------------------------------------------------------ :  -
LpMDHk47  : ------------------------------------------------------------ :  -
LpMDHk48  : ------------------------------------------------------------ :  -
LpMDHk49  : ------------------------------------------------------------ :  -
LpMDHk50  : ------------------------------------------------------------ :  -
LpMDHk51  : ------------------------------------------------------------ :  -
LpMDHk52  : ------------------------------------------------------------ :  -
LpMDHk53  : ------------------------------------------------------------ :  -
LpMDHk54  : ------------------------------------------------------------ :  -
LpMDHk55  : ------------------------------------------------------------ :  -
LpMDHk56  : ------------------------------------------------------------ :  -
LpMDHk57  : ------------------------------------------------------------ :  -
LpMDHk58  : ------------------------------------------------------------ :  -
LpMDHk59  : ------------------------------------------------------------ :  -
LpMDHk60  : ------------------------------------------------------------ :  -
LpMDHk61  : ------------------------------------------------------------ :  -
LpMDHk62  : ------------------------------------------------------------ :  -
LpMDHk63  : ------------------------------------------------------------ :  -
LpMDHk64  : ------------------------------------------------------------ :  -
LpMDHk65  : ------------------------------------------------------------ :  -
LpMDHk66  : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 714
```

```
                      *        1220         *        1240         *        1260
LpMDHk1    : ------------------------------------------------------------ :   -
LpMDHk2    : ------------------------------------------------------------ :   -
LpMDHk3    : ------------------------------------------------------------ :   -
LpMDHk4    : ------------------------------------------------------------ :   -
LpMDHk5    : ------------------------------------------------------------ :   -
LpMDHk6    : ------------------------------------------------------------ :   -
LpMDHk7    : ------------------------------------------------------------ :   -
LpMDHk8    : ------------------------------------------------------------ :   -
LpMDHk9    : ------------------------------------------------------------ :   -
LpMDHk10   : ------------------------------------------------------------ :   -
LpMDHk11   : ------------------------------------------------------------ :   -
LpMDHk12   : ------------------------------------------------------------ :   -
LpMDHk13   : ------------------------------------------------------------ :   -
LpMDHk14   : ------------------------------------------------------------ :   -
LpMDHk15   : ------------------------------------------------------------ :   -
LpMDHk16   : ------------------------------------------------------------ :   -
LpMDHk17   : ------------------------------------------------------------ :   -
LpMDHk18   : ------------------------------------------------------------ :   -
LpMDHk19   : ------------------------------------------------------------ :   -
LpMDHk20   : ------------------------------------------------------------ :   -
LpMDHk21   : ------------------------------------------------------------ :   -
LpMDHk22   : ------------------------------------------------------------ :   -
LpMDHk23   : ------------------------------------------------------------ :   -
LpMDHk24   : ------------------------------------------------------------ :   -
LpMDHk25   : ------------------------------------------------------------ :   -
LpMDHk26   : ------------------------------------------------------------ :   -
LpMDHk27   : ------------------------------------------------------------ :   -
LpMDHk28   : ------------------------------------------------------------ :   -
LpMDHk29   : ------------------------------------------------------------ :   -
LpMDHk30   : ------------------------------------------------------------ :   -
LpMDHk31   : ------------------------------------------------------------ :   -
LpMDHk32   : ------------------------------------------------------------ :   -
LpMDHk33   : ------------------------------------------------------------ :   -
LpMDHk34   : ------------------------------------------------------------ :   -
LpMDHk35   : ------------------------------------------------------------ :   -
LpMDHk36   : ------------------------------------------------------------ :   -
LpMDHk37   : ------------------------------------------------------------ :   -
LpMDHk38   : ------------------------------------------------------------ :   -
LpMDHk39   : ------------------------------------------------------------ :   -
LpMDHk40   : ------------------------------------------------------------ :   -
LpMDHk41   : ------------------------------------------------------------ :   -
LpMDHk42   : ------------------------------------------------------------ :   -
LpMDHk43   : ------------------------------------------------------------ :   -
LpMDHk44   : ------------------------------------------------------------ :   -
LpMDHk45   : ------------------------------------------------------------ :   -
LpMDHk46   : ------------------------------------------------------------ :   -
LpMDHk47   : ------------------------------------------------------------ :   -
LpMDHk48   : ------------------------------------------------------------ :   -
LpMDHk49   : ------------------------------------------------------------ :   -
LpMDHk50   : ------------------------------------------------------------ :   -
LpMDHk51   : ------------------------------------------------------------ :   -
LpMDHk52   : ------------------------------------------------------------ :   -
LpMDHk53   : ------------------------------------------------------------ :   -
LpMDHk54   : ------------------------------------------------------------ :   -
LpMDHk55   : ------------------------------------------------------------ :   -
LpMDHk56   : ------------------------------------------------------------ :   -
LpMDHk57   : ------------------------------------------------------------ :   -
LpMDHk58   : ------------------------------------------------------------ :   -
LpMDHk59   : ------------------------------------------------------------ :   -
LpMDHk60   : ------------------------------------------------------------ :   -
LpMDHk61   : ------------------------------------------------------------ :   -
LpMDHk62   : ------------------------------------------------------------ :   -
LpMDHk63   : ------------------------------------------------------------ :   -
LpMDHk64   : ------------------------------------------------------------ :   -
LpMDHk65   : ------------------------------------------------------------ :   -
LpMDHk66   : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG :  774
```

LpMDHk1	---	-
LpMDHk2	---	-
LpMDHk3	---	-
LpMDHk4	---	-
LpMDHk5	---	-
LpMDHk6	---	-
LpMDHk7	---	-
LpMDHk8	---	-
LpMDHk9	---	-
LpMDHk10	---	-
LpMDHk11	---	-
LpMDHk12	---	-
LpMDHk13	---	-
LpMDHk14	---	-
LpMDHk15	---	-
LpMDHk16	---	-
LpMDHk17	---	-
LpMDHk18	---	-
LpMDHk19	---	-
LpMDHk20	---	-
LpMDHk21	---	-
LpMDHk22	---	-
LpMDHk23	---	-
LpMDHk24	---	-
LpMDHk25	---	-
LpMDHk26	---	-
LpMDHk27	---	-
LpMDHk28	---	-
LpMDHk29	---	-
LpMDHk30	---	-
LpMDHk31	---	-
LpMDHk32	---	-
LpMDHk33	---	-
LpMDHk34	---	-
LpMDHk35	---	-
LpMDHk36	---	-
LpMDHk37	---	-
LpMDHk38	---	-
LpMDHk39	---	-
LpMDHk40	---	-
LpMDHk41	---	-
LpMDHk42	---	-
LpMDHk43	---	-
LpMDHk44	---	-
LpMDHk45	---	-
LpMDHk46	---	-
LpMDHk47	---	-
LpMDHk48	---	-
LpMDHk49	---	-
LpMDHk50	---	-
LpMDHk51	---	-
LpMDHk52	---	-
LpMDHk53	---	-
LpMDHk54	---	-
LpMDHk55	---	-
LpMDHk56	---	-
LpMDHk57	---	-
LpMDHk58	---	-
LpMDHk59	---	-
LpMDHk60	---	-
LpMDHk61	---	-
LpMDHk62	---	-
LpMDHk63	---	-
LpMDHk64	---	-
LpMDHk65	---	-
LpMDHk66	AAG	777

re 38 Nucleotide sequence of LpMDH1

```
                    *        20         *        40         *        60
LpMDH1 : GNAAACAGNNGCGNCTTTTCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA :  60

                    *        80         *       100         *       120
LpMDH1 : TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCTGGTA : 120

                    *       140         *       160         *       180
LpMDH1 : CGTTTGATGTATTAGTGATGCCAAATCTATATGGCGACATTATTAGTGATCTATGTGCTG : 180

                    *       200         *       220         *       240
LpMDH1 : GTTTGATCGGAGGCTTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTTGTC : 240

                    *       260         *       280         *       300
LpMDH1 : TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGAACCTGGCAAACCCAA : 300

                    *       320         *       340         *       360
LpMDH1 : CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCGCCACTTGCAATTNAACGACCAAGCAN : 360

                    *       380         *       400         *
LpMDH1 : AACGGATCCACAATGCTATCCTCCAGACTATCGNCGAGGGGAAGNACANAACTG : 414
```

re 39 Deduced amino acid sequence of LpMDH1

```
                  *         20          *         40          *         60
LpMDH1 : KQXXLFXXCCRAIAXKYPEIIYEEVIIDNCCMTLVKNPGTFDVLVMPNLYGDIISDLCAG :  60

                  *         80          *        100          *        120
LpMDH1 : LIGGLGLTPSCNIGEGGICLAEAVHGSAPDISGKNLANPTALMLSAVMMLRHLQXNDQAX : 120

                  *
LpMDH1 : RIHNAILQTIXEGKXXT : 137
```

re 40   Nucleotide sequence of LpMDHm

```
                    *        20         *        40         *        60
LpMDHm : GNCACCNCCAGNNACAACTCTGGTACCTCAATTGCTACTCCACACCTCACTACTTCTACC :  60

                    *        80         *       100         *       120
LpMDHm : AATCCACTACACAGCTTCGAGCTACCCCGCCCCCGCAATCCAAACTACCTCTCCCTAGCA : 120

                    *       140         *       160         *       180
LpMDHm : AATCTACAACATGAAGGCAGTCGTAGCTGGAGCCGCCGGTGGCATTGGACAGCCATTGTC : 180

                    *       200         *       220         *       240
LpMDHm : CCTCCTCCTTAAGACCTGCCCGCTCGTCACTGAGCTCGCCCTATACGATGTCGTCAACGC : 240

                    *       260         *       280         *       300
LpMDHm : CGTCGGTGTCGCGACTGACCTCTCCCACATCTCCTCGCCCGCGAAAGTAACCGGCTACCT : 300

                    *       320         *       340         *       360
LpMDHm : GCCGGCAAATGACGGTATGCAGCAGGCTCTCACTGGCGCCGACATCGTGGTCATCCCCGC : 360

                    *       380         *       400         *       420
LpMDHm : TGGTATTCCCCGCAAGCCCGGCATGACCCGTGACGACCTCTTCAAGATCAACGCCGGCAT : 420

                    *       440         *       460         *       480
LpMDHm : TGTCCAGGGTCTCATCGAGGGTGTCGCCAAGCACTGCCCCAAGGCATACGTTCTCGTCAT : 480

                    *       500         *       520         *       540
LpMDHm : CTCCAACCCCGTCAACTCGACTGTGCCCATCGCCGCCGAGGTGCTGAAGAAGGCCGGTGT : 540

                    *       560         *       580         *       600
LpMDHm : CTTCGACCCCAAGAAGCTCTTCGGTGTCACCACCCTCGATGTCGTCCGCGCCGAGACCTT : 600

                    *       620         *       640         *
LpMDHm : CGTTGCCGAGATCACTGGCGAGAAGGACCCAGCGAAGTTGAACATNCCCGTA : 652
```

re 41   Deduced amino acid sequence of LpMDHm

```
                    *        20         *        40         *        60
LpMDHm : XXPXTTLVPQLLLHTSLLLPIHYTASSYPAPAIQTTSP*QIYNMKAVVAGAAGGIGQPLS :  59

                    *        80         *       100         *       120
LpMDHm : LLLKTCPLVTELALYDVVNAVGVATDLSHISSPAKVTGYLPANDGMQQALTGADIVVIPA : 119

                    *       140         *       160         *       180
LpMDHm : GIPRKPGMTRDDLFKINAGIVQGLIEGVAKHCPKAYVLVISNPVNSTVPIAAEVLKKAGV : 179

                    *       200         *
LpMDHm : FDPKKLFGVTTLDVVRAETFVAEITGEKDPAKLNXPV : 216
```

ure 42 Nucleotide sequence of LpPEPCa

```
                      *        20         *        40         *        60
LpPEPCa : GNGTACACGAAATAGAATCAACGGAAAGCANGAAGTGATGATTGGGTATCAGCATTCTGG :  60

                      *        80         *       100         *       120
LpPEPCa : GAAGGATGCTGGCCGTTTCTCTGCTGGTTGGCACTTGTACAAAGCTCAAGAGGAGCTTAT : 120

                      *       140         *       160         *       180
LpPEPCa : TAAGGTTGCGGAGACGTTTGGGGTTAAGNTGACTATGTTTCATGGACGAGGGGGTACTGT : 180

                      *       200         *       220         *       240
LpPEPCa : TGGAAGAGGTGGCGGCCCTACCCATCTTGCTATACTGTCACAACCTCCAGATACTGTCCA : 240

                      *       260         *       280         *       300
LpPEPCa : TGGATCACTTCGGGTAACTGTTCAAGGTGAAGTCATTGAGCAGTCCTTCGGAGAGGAGCA : 300

                      *       320         *       340         *       360
LpPEPCa : TTTGTGTTTTAGAACGCTTCAACGTTTTACAGCTGCTACTCTTGAACATGGTATGCATCC : 360

                      *       380         *       400         *       420
LpPEPCa : ACCAATCTCACCTAAACCAGAATGGCGTGCTTTGATGGATGAAATGGCTGTTGTTGCCAC : 420

                      *       440         *       460         *       480
LpPEPCa : AGAGGAATACCGTTCCATTGTTTTCCAAGAACCAAGATTTGTTGAGTATTTCCGCCTTGC : 480

                      *       500         *       520         *       540
LpPEPCa : AACACCAGAGCTCGAGTATGGTAGGATGAATATTGGAAGCAGGCCATCAAAACGTAAGCC : 540

                      *       560         *       580         *       600
LpPEPCa : AAGCGGAGGAATCGAATCATTGCGTGCAATTCCTTGGATATTTGCTTGGACACAGACTAG : 600

                      *       620         *       640         *       660
LpPEPCa : ATTCCACCTGCCAGTGTGGCTTGNTTTTGGTGCGGCCTTCAAGCATGTCCTGCAAAAGGA : 660

                      *       680         *       700         *       720
LpPEPCa : CATTCGTANTCTTCAAATCCTTCAGCAGATGTACAACGAGTGGCCGTTTAGGGTTACCAT : 720

                      *       740         *       760
LpPEPCa : AAACCTGGTTGAGATGGTGTTTGCCAAGGGCGATCCAGGTATAGCAGCT : 769
```

re 43   Deduced amino acid sequence of LpPEPca

```
                     *        20         *        40         *        60
LpPEPca : XTRNRINGKXEVMIGYQHSGKDAGRFSAGWHLYKAQEELIKVAETFGVKXTMFHGRGGTV :  60

                     *        80         *       100         *       120
LpPEPca : GRGGGPTHLAILSQPPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHP : 120

                     *       140         *       160         *       180
LpPEPca : PISPKPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSRPSKRKP : 180

                     *       200         *       220         *       240
LpPEPca : SGGIESLRAIPWIFAWTQTRFHLPVWLXFGAAFKHVLQKDIRXLQILQQMYNEWPFRVTI : 240

                     *
LpPEPca : NLVEMVFAKGDPGIAA : 256
```

ure 44 Consensus contig nucleotide sequence of LpPEPCb

```
                     *        20         *        40         *        60
LpPEPCb : GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGCAGAGCTCCCAGCAGATTGTT :  60

                     *        80         *       100         *       120
LpPEPCb : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120

                     *       140         *       160         *       180
LpPEPCb : TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTG : 180

                     *       200         *       220         *       240
LpPEPCb : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA : 240

                     *       260         *       280         *       300
LpPEPCb : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG : 300

                     *       320         *       340         *       360
LpPEPCb : GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 360

                     *       380         *       400         *       420
LpPEPCb : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420

                     *       440         *       460         *       480
LpPEPCb : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 480

                     *       500         *       520         *       540
LpPEPCb : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 540

                     *       560         *       580         *       600
LpPEPCb : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 600

                     *       620         *       640         *       660
LpPEPCb : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 660

                     *       680         *       700         *       720
LpPEPCb : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 720

                     *       740         *       760         *       780
LpPEPCb : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 780

                     *       800         *       820         *       840
LpPEPCb : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 840

                     *       860         *       880         *       900
LpPEPCb : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 900

                     *       920         *       940         *       960
LpPEPCb : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 960
```

```
                    *        980          *        1000          *        1020
LpPEPCb : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 1020

                    *        1040         *        1060          *        1080
LpPEPCb : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 1080

                    *        1100         *        1120          *        1140
LpPEPCb : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 1140

                    *        1160         *        1180          *        1200
LpPEPCb : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCNACACCC : 1200

                    *        1220         *        1240          *        1260
LpPEPCb : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 1260

                    *        1280         *        1300          *        1320
LpPEPCb : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 1320

                    *        1340         *        1360          *        1380
LpPEPCb : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 1380

                    *        1400         *        1420          *        1440
LpPEPCb : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGATGGGGCGTGA : 1440

                    *        1460         *        1480          *        1500
LpPEPCb : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 1500

                    *        1520         *        1540          *        1560
LpPEPCb : TTGGTTATGGATGNACTTTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 1560

                    *        1580         *        1600          *        1620
LpPEPCb : ATATGGAACAATGATATTCTGGTNGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 1620

                    *        1640
LpPEPCb : GNGATTTGGAGTNGTTTAAC : 1640
```

Figure 45 Deduced amino acid sequence of LpPEPCb

```
                    *        20         *        40         *        60
LpPEPCb : RSCXCFKXIXVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKKPLRVVPLFEKLA :  60

                    *        80         *       100         *       120
LpPEPCb : DLEXAPASVARLFSIDWYMNRINGKQEVMIGYSDSGKDAGRLSAAWQMYKAQEDLIKVAK : 120

                    *       140         *       160         *       180
LpPEPCb : QYGVKLTMFHGRGGTVGRGGGPSHLAILSQPPDTIQGSLRVTVQGEVIEHSFGEEHLCFR : 180

                    *       200         *       220         *       240
LpPEPCb : TLQRFTAATLEHGMHPPISPKPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSATPET : 240

                    *       260         *       280         *       300
LpPEPCb : EYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI : 300

                    *       320         *       340         *       360
LpPEPCb : HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSEDLQPFGEQLRNNFEETKQ : 360

                    *       380         *       400         *       420
LpPEPCb : LLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPLSKE : 420

                    *       440         *       460
LpPEPCb : FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG : 462
```

Figure 46 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpPEPCb

```
                    *        20         *        40         *        60
LpPEPCb1 : GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGCAGAGCTCCCAGCAGATTGTT :  60
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
LpPEPCb1 : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       140         *       160         *       180
LpPEPCb1 : TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTG : 180
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       200         *       220         *       240
LpPEPCb1 : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA : 240
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       260         *       280         *       300
LpPEPCb1 : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG : 300
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       320         *       340         *       360
LpPEPCb1 : GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 360
LpPEPCb2 : -------------------------GTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA :  35
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       380         *       400         *       420
LpPEPCb1 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420
LpPEPCb2 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG :  95
LpPEPCb3 : ----------------------AATGTTT-NTGGAAGAGGTGGAACGGTTGGCAGAGGAG :  37
LpPEPCb4 : ---------------------------------------------------GCANAGGAG :   9
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -
```

```
                       *       440         *       460         *       480
LpPEPCb1 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 480
LpPEPCb2 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 155
LpPEPCb3 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACTAGACACGATACAAGGATCACTTC :  97
LpPEPCb4 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC :  69
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       500         *       520         *       540
LpPEPCb1 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 540
LpPEPCb2 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGGGGAACACTTGTGCTTCA : 215
LpPEPCb3 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 157
LpPEPCb4 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 129
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       560         *       580         *       600
LpPEPCb1 : NAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCGC : 600
LpPEPCb2 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 275
LpPEPCb3 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 217
LpPEPCb4 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 189
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       620         *       640         *       660
LpPEPCb1 : CCAAACCAGAATGGCNTGCTATAATGGATGANATGGCTGTAGNGGCACCAAAAGAAAATC : 660
LpPEPCb2 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 335
LpPEPCb3 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 277
LpPEPCb4 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 249
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       680         *       700         *       720
LpPEPCb1 : GATCAATTGNCTTCCAAGAACCGCNTTTTGNCNAATA----------------------- : 697
LpPEPCb2 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 395
LpPEPCb3 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 337
LpPEPCb4 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 309
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       740         *       760         *       780
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455
LpPEPCb3 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397
LpPEPCb4 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 369
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       800         *       820         *       840
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515
LpPEPCb3 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC : 457
LpPEPCb4 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -
```

```
                 *        860         *        880         *        900
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 575
LpPEPCb3 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 517
LpPEPCb4 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 489
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                 *        920         *        940         *        960
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 635
LpPEPCb3 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 577
LpPEPCb4 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 549
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                 *        980         *       1000         *       1020
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 695
LpPEPCb3 : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGGATTGCTGCTTTATATGACAAATTGCTTG : 637
LpPEPCb4 : TTGAGATGGTTTTTGCCGAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 609
LpPEPCb5 : -------GGTTTTTG-CNAGGGAGATCC-GG-ATTGCTGCTTTATATGACAAATTGCTTG :  50
LpPEPCb6 : ------------------------------------------------------------ :   -

                 *       1040         *       1060         *       1080
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGANAAACAACTTTGAAGAGACGAAAC : 755
LpPEPCb3 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 697
LpPEPCb4 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 669
LpPEPCb5 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCNGCTGAGAAACAACTTTGAAGAGACGAAAC : 110
LpPEPCb6 : ------------------------------------------------------------ :   -

                 *       1100         *       1120         *       1140
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : AGNTACTCTTTAAGGTTGTTGNCCACAAGG------------------------------ : 785
LpPEPCb3 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 757
LpPEPCb4 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGACGGGGATCCTTACCTGAAGC : 729
LpPEPCb5 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 170
LpPEPCb6 : ----------------------------GGACGTTCTTGAAGGGGATCCTTACCTGAAGC :  32

                 *       1160         *       1180         *       1200
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : AGCGTCTGCGGGTGCGTGAGTCATAC---------------------------------- : 783
LpPEPCb4 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACA------------------------- : 764
LpPEPCb5 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCTACACCC : 230
LpPEPCb6 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCGNNCACCC :  92

                 *       1220         *       1240         *       1260
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 290
LpPEPCb6 : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 152
```

```
                      *        1280         *        1300         *        1320
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 350
LpPEPCb6 : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 212

                      *        1340         *        1360         *        1380
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTA-TTGCTGTGGAATGCAAA : 409
LpPEPCb6 : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 272

                      *        1400         *        1420         *        1440
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ACACAGGCTAGGCCAGTTTGCCTA-TTGGAATAACTGTCATTCCGTCAGATGGGGCGTGA : 468
LpPEPCb6 : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGAT-GGGCGTGA : 331

                      *        1460         *        1480         *        1500
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 528
LpPEPCb6 : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCA-TTTGGCCACTTACATGCCTT : 390

                      *        1520         *        1540         *        1560
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : TTGGTTATGNATGNAC-TTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 587
LpPEPCb6 : TTGGTTATGGATGNACTTTGATCTTAATGTCAANGGTTGTTGAAGCCTGATCTAAATNAA : 450

                      *        1580         *        1600         *        1620
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ATATGGAACAATGATATTCTGG-NGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 646
LpPEPCb6 : ATATGGAACAATGATATTCTGGTTGTTTCTTA---------------------------- : 482

                      *        1640
LpPEPCb1 : -------------------- :   -
LpPEPCb2 : -------------------- :   -
LpPEPCb3 : -------------------- :   -
LpPEPCb4 : -------------------- :   -
LpPEPCb5 : GNGATTTGGAGTNGTTTAAC : 666
LpPEPCb6 : -------------------- :   -
```

ure 47 Nucleotide sequence of LpPEPCc

```
                        *        20         *        40         *        60
LpPEPCc : AGCANTCTGTNCTTNCCANCAACCACGTTTTGTNCGAATACTTNCCGCTCGGCAACACCT :  60

                        *        80         *       100         *       120
LpPEPCc : GCACACTGAATATGGTCGGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTG : 120

                        *       140         *       160         *       180
LpPEPCc : GAGGCATAGAATCGCTCCGTGCAATTCCATGCATCTTTGNTTGGACACAGACAAGGNTTN : 180

                        *       200         *       220
LpPEPCc : ATNTTCCTGTATGNCTTGNATTCGNCTCCACCNCCACCCCCNTA : 224
```

Figure 48 Deduced amino acid sequence of LpPEPCc

```
                    *        20         *        40         *        60
LpPEPCc : XSXLXXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIPCIFXWTQTRXX : 60

                    *
LpPEPCc : XPVXLXFXSTXTP : 73
```

...ure 49   Nucleotide sequence of LpPEPCd

```
                       *        20         *        40         *        60
LpPEPCd : GTTNCTGGAACNAAGGATCTTCTTGAAGGTGATCCCTACCTGAAGCAGCGGCTCCGCCTC :  60

                       *        80         *       100         *       120
LpPEPCd : CGTGACGCGTACATCACCACCATGAACGTATGCCAGGCCTACACATTGAAGCGGATCCGT : 120

                       *       140         *       160         *       180
LpPEPCd : GACCCAGACTACCACGTCGCACTGCGGCCCCATCTTTCCAAGGAGGTTATGGACACAAGC : 180

                       *       200         *       220         *       240
LpPEPCd : AAGCCGGCTTCCGAGCTTGTGACGCTGAACCCGGCCAGCGAGTACGCCCCGGGGCTGGAG : 240

                       *       260         *       280         *       300
LpPEPCd : GACACCCTCATCTTGACCATGAAGGGCGTTGCTGCCGGTCTGCAAAACACCGGTTAGGGC : 300

                       *       320         *       340         *       360
LpPEPCd : CAGGAGAGATGCCTGATCACCATCTTTTTGTATCTTCATGATGATGCGATGTTTTTCTTT : 360

                       *       380         *       400         *       420
LpPEPCd : AGTCGTTTGCGGTGGGCCTTATATCTCTCGGACGTAGCTGCATCTGTCTCCCTGCTCAGT : 420

                       *       440         *       460         *       480
LpPEPCd : GAGGAATAATGGCGTTTCGCCCAAGTATATTGATAAATAAAGGGAACCGATGTTAATTTC : 480

                       *       500         *       520
LpPEPCd : AGATTTGTTTGTTAGTAATTGTTCTATTTATTTTGCGAAAAAAAAAA : 527
```

Figure 50 Deduced amino acid sequence of LpPEPCd

```
                    *        20         *        40         *        60
LpPEPCd : VXGXKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTLKRIRDPDYHVALRPHLSKEVMDTS : 60

                    *        80         *
LpPEPCd : KPASELVTLNPASEYAPGLEDTLILTMKGVAAGLQNTG : 98
```

Figure 51 Nucleotide sequence of LpPEPCe

```
                      *        20         *        40         *        60
LpPEPCe : GTTACACGCGCAGTTTGCTTGTTAGCAAGGNAGATGGCTGCTAACTTGTACTTCTCTCAG :  60

                      *        80         *       100         *       120
LpPEPCe : ATAGAAGATCTGATGTTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT : 120

                      *       140         *       160         *       180
LpPEPCe : GCAGATGAAGTACATCTGTCCTCAAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG : 180

                      *       200         *       220         *       240
LpPEPCe : AAGCAAGTTCCTCCAAATGAACCTTATCGTGTCATACTTGGCGATGTCAGGGATAAACTG : 240

                      *       260         *       280         *       300
LpPEPCe : TACTATACGCGCGAACGTTCTCGCCACATATTGACAACTGGAATTTCAGACATTCCAGAA : 300

                      *       320         *       340         *       360
LpPEPCe : GNGTCAACTTTTACTAATGTTGAACTGTTTCTGGAACCTCTTGAGCTGTGCTACAGATCC : 360

                      *       380         *       400         *       420
LpPEPCe : TTATCTTNCTGTGGNGACAAANCTATTGCTGANGGAAGCCTTCTTGATTTCTNGCGNNCN : 420

                      *       440         *
LpPEPCe : GNATCNACTTTGTGGGCTTACTCTNGCGAA : 450
```

ure 52   Deduced amino acid sequence of LpPEPCe

```
                       *        20         *        40         *        60
LpPEPCe : VTRAVCLLARXMAANLYFSQIEDLMFELSMWRCSDELRVRADEVHLSSKKKSAKHYIEFW :  60

                       *        80         *       100         *       120
LpPEPCe : KQVPPNEPYRVILGDVRDKLYYTRERSRHILTTGISDIPEXSTFTNVELFLEPLELCYRS : 120

                       *       140         *
LpPEPCe : LSXCXDKXIAXGSLLDFXXXXXTLWAYSXE : 150
```

ure 53 Nucleotide sequence of LpPEPCf

```
                          *        20         *        40         *        60
LpPEPCf : GGGGTGGTGGCCCTNCTCACCTTGCCTNCCTGTCTCANCCACCAGNCACAATCAACGGAT :  60

                          *        80         *       100         *       120
LpPEPCf : CACTCCGGGTGACTGTTCAAGGTGAAGTTATTGAGCAGAGCTTTGGGGAGGAACACTTGT : 120

                          *       140         *       160         *       180
LpPEPCf : GCTTCAGGACGCTGCAGCGTTTCACAGCTGCTACTCTTGAGCATGGGATGCGTCCACCCA : 180

                          *       200         *       220         *       240
LpPEPCf : TTTCACCAAAGCCAGAGTGGCGAGCTCTTCTTGATGAGATGGCTGTGGTTGCAACTGAGG : 240

                          *       260         *       280         *       300
LpPEPCf : AATACCGGTCAATCGTCTTCCAAGAACCACGCTTCGTCGAGTATTTCCGCCTTGCAACAC : 300

                          *       320         *       340         *       360
LpPEPCf : CAGAGACAGAGTATGGCAGGATGAATATAGGAAGCAGGCCATCAAAGAGAAAACCAAGTG : 360

                          *       380         *       400         *       420
LpPEPCf : GTGGCATTGAATCACTCCGTGCAATTCCATGGATCTTCGCATGGACGCAGACACGGTTCC : 420

                          *       440         *       460         *       480
LpPEPCf : ACCTTCCAGTCTGGTTGGGCTTTGGTGGTGCATTCAAGCATATCCTCAAGAAGGACATCA : 480

                          *       500         *       520         *       540
LpPEPCf : GAAATTTCCATATGCTCCAGGAGATGTACAACGAGTGGCCATTTTTCAGGGTCACGATCG : 540

                          *       560         *       580         *       600
LpPEPCf : ATCTTGTTGAGATGGTGTTCGCCAAGGGTAACCCTGGCATTGCTGCCTTGTATGACAGGC : 600

                          *       620         *       640
LpPEPCf : TCCTGGTTTCAGAGGAGCTACAGCCACTGGGTGACAAGCTGAGG : 644
```

ure 54 Deduced amino acid sequence of LpPEPCf

```
                         *        20         *        40         *        60
LpPEPCf : GGGPXHLAXLSXPPXTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPI :  60

                         *        80         *       100         *       120
LpPEPCf : SPKPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSRPSKRKPSG : 120

                         *       140         *       160         *       180
LpPEPCf : GIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNFHMLQEMYNEWPFFRVTID : 180

                         *       200         *
LpPEPCf : LVEMVFAKGNPGIAALYDRLLVSEELQPLGDKLR : 214
```

Figure 55 Consensus contig nucleotide sequence of TrMDHa

```
                  *        20         *        40         *        60
TrMDHa : GGCTTCTTAAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  60

                  *        80         *       100         *       120
TrMDHa : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 120

                  *       140         *       160         *       180
TrMDHa : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 180

                  *       200         *       220         *       240
TrMDHa : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 240

                  *       260         *       280         *       300
TrMDHa : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 300

                  *       320         *       340         *       360
TrMDHa : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 360

                  *       380         *       400         *       420
TrMDHa : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 420

                  *       440         *       460         *       480
TrMDHa : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 480

                  *       500         *       520         *       540
TrMDHa : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 540

                  *       560         *       580         *       600
TrMDHa : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 600

                  *       620         *       640         *       660
TrMDHa : AATGTTATAATATGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC : 660

                  *
TrMDHa : CGTTAAAATCTCCT : 674
```

Figure 56 Deduced amino acid sequence of TrMDHa

```
                  *        20         *        40         *        60
TrMDHa : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD :  60

                  *        80         *       100         *       120
TrMDHa : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMTKNVSIYKSQASALEKH : 120

                  *       140         *       160         *       180
TrMDHa : AAANCKVLVVANPANTNALILKEYAPSIPEKNISALTRLDHNRALGQISERLNVEVSDVK : 180

                  *       200
TrMDHa : NVIIWGKXFINSIPXCXPXNR : 201
```

Figure 57 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHa

```
                        *        20         *        40         *        60
TrMDHa1  : GTNTTCTTGNAAACNCNCTAATNTCTTTTCTATTGTNCTNNTTTCTTCGATCTATTTCCA :  60
TrMDHa2  : -GCNACNTATAACCTCTTTNTNCTNACGTCTATTGTTCTTATTTCTTCGATCTATATCCA :  59
TrMDHa3  : -GCNTCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  57
TrMDHa4  : -GCATCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  57
TrMDHa5  : --CTTCTT-NAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC- :  55
TrMDHa6  : -----CNTTAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTT-CN :  54
TrMDHa7  : --------------GCANTAAACTCTTTTNTATTGTTCTTNTTTCTTCGATCTATTTCC- :  45
TrMDHa8  : --------------GCANTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC- :  45
TrMDHa9  : ---------------CACT-AACTCTTTTCT-TTGTTCTTNTTTCTTCGATC-ATTTCC- :  41
TrMDHa10 : ------------------TAAACTCTTNTCTATTGTTCTTNTTTCTTCGATCTATTTCC- :  41
TrMDHa11 : -------------------AAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  41

                        *        80         *       100         *       120
TrMDHa1  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCNCTGGTGCTGCAGGACAACTTGGGTATGCT : 120
TrMDHa2  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 119
TrMDHa3  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa4  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa5  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 115
TrMDHa6  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 114
TrMDHa7  : ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 104
TrMDHa8  : ATGGCC-AAGACCCAGTTCGTGTTCTTGT-CCTGGTGCTGCAGGACAAATTGGGTATGCT : 103
TrMDHa9  : ATGGCC-AAGACCCAGTTCGTGTTCTTGT-ACTGGTGCTGCAGGACAACTTGGGTATGCT :  99
TrMDHa10 : ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 100
TrMDHa11 : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 101

                        *       140         *       160         *       180
TrMDHa1  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC : 180
TrMDHa2  : CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 179
TrMDHa3  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa4  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa5  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 175
TrMDHa6  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 174
TrMDHa7  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 164
TrMDHa8  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 163
TrMDHa9  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 159
TrMDHa10 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 160
TrMDHa11 : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 161

                        *       200         *       220         *       240
TrMDHa1  : ATGCTTGACATTNCACCTGGAG-------------------------------------- : 202
TrMDHa2  : ATGCTTGACATCCCACCTGCAGCCGAATCACTGAACGGTGTAAAAATGGAGTTGGTGGAT : 239
TrMDHa3  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa4  : ATGCTTGACATTCCACCTGCAGCCGAATCACTGAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa5  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 235
TrMDHa6  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 234
TrMDHa7  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 224
TrMDHa8  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 223
TrMDHa9  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 219
TrMDHa10 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 220
TrMDHa11 : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 221
```

```
                  *        260         *        280         *        300
TrMDHa1  : ------------------------------------------------------------ :  -
TrMDHa2  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCACT : 299
TrMDHa3  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 297
TrMDHa4  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 297
TrMDHa5  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 295
TrMDHa6  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 294
TrMDHa7  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 284
TrMDHa8  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 283
TrMDHa9  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 279
TrMDHa10 : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 280
TrMDHa11 : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 281

                  *        320         *        340         *        360
TrMDHa1  : ------------------------------------------------------------ :  -
TrMDHa2  : GGGGTCAATATTGCCGTTATGGTTGGGGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 359
TrMDHa3  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 357
TrMDHa4  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 357
TrMDHa5  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 355
TrMDHa6  : GGTGTNAATATTGACGNTATGGNTGGNGGGTTNCNTAGNANACAAGGTNT---------- : 344
TrMDHa7  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 344
TrMDHa8  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 343
TrMDHa9  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 339
TrMDHa10 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 340
TrMDHa11 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTANAAAAGAANGTATGGAGAGGAAA : 341

                  *        380         *        400         *        420
TrMDHa1  : ------------------------------------------------------------ :  -
TrMDHa2  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 419
TrMDHa3  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 417
TrMDHa4  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 417
TrMDHa5  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 415
TrMDHa6  : ------------------------------------------------------------ :  -
TrMDHa7  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 404
TrMDHa8  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 403
TrMDHa9  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 399
TrMDHa10 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 400
TrMDHa11 : GATGTGATGAC-AAAAATGTCTCTATTTACAAGTCTTAAGCTTTTGNCCTTGAAAAACAT : 400

                  *        440         *        460         *        480
TrMDHa1  : ------------------------------------------------------------ :  -
TrMDHa2  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 479
TrMDHa3  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 477
TrMDHa4  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 477
TrMDHa5  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 475
TrMDHa6  : ------------------------------------------------------------ :  -
TrMDHa7  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 464
TrMDHa8  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 463
TrMDHa9  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 459
TrMDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 460
TrMDHa11 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGNCAACCCACCAAACACCAATGCATTGATC : 460
```

```
                           *        500         *        520         *        540
TrMDHa1  : ------------------------------------------------------------ :   -
TrMDHa2  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 539
TrMDHa3  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 537
TrMDHa4  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 537
TrMDHa5  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 535
TrMDHa6  : ------------------------------------------------------------ :   -
TrMDHa7  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 524
TrMDHa8  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 523
TrMDHa9  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 519
TrMDHa10 : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 520
TrMDHa11 : TTGAAGGAATATGCTCCATNCATTCCTGANAAAAACATTTNTGCTTTGACTAGATTGGAC : 520

                           *        560         *        580         *        600
TrMDHa1  : ------------------------------------------------------------ :   -
TrMDHa2  : CATAACAGGGCACTTGGTCA---------------------------------------- : 559
TrMDHa3  : CATAACAGGGCACTAGGTCAAATTTCTGAA------------------------------ : 567
TrMDHa4  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAA---------------------- : 575
TrMDHa5  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 595
TrMDHa6  : ------------------------------------------------------------ :   -
TrMDHa7  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGAC-------------------------- : 558
TrMDHa8  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 583
TrMDHa9  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGG-- : 577
TrMDHa10 : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 580
TrMDHa11 : CATAACAGGGCACTAGGGCAAATTTNTGAAANACTAAACGTTGAAGTTTNTGATGTGAAA : 580

                           *        620         *        640         *        660
TrMDHa1  : ------------------------------------------------------------ :   -
TrMDHa2  : ------------------------------------------------------------ :   -
TrMDHa3  : ------------------------------------------------------------ :   -
TrMDHa4  : ------------------------------------------------------------ :   -
TrMDHa5  : AATGTTAT-A-AT----------------------------------------------- : 606
TrMDHa6  : ------------------------------------------------------------ :   -
TrMDHa7  : ------------------------------------------------------------ :   -
TrMDHa8  : AATGTTATAATCTGGG-------------------------------------------- : 599
TrMDHa9  : ------------------------------------------------------------ :   -
TrMDHa10 : AATGTTATAATCTG---------------------------------------------- : 594
TrMDHa11 : AATGTTAT-ATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC : 639

                           *
TrMDHa1  : -------------- :   -
TrMDHa2  : -------------- :   -
TrMDHa3  : -------------- :   -
TrMDHa4  : -------------- :   -
TrMDHa5  : -------------- :   -
TrMDHa6  : -------------- :   -
TrMDHa7  : -------------- :   -
TrMDHa8  : -------------- :   -
TrMDHa9  : -------------- :   -
TrMDHa10 : -------------- :   -
TrMDHa11 : CGTTAAAATCTCCT : 653
```

Figure 58 Consensus contig nucleotide sequence of TrMDHb

```
                   *        20         *        40         *        60
TrMDHb : TTCTCCCANAATCNNGAAANCGCCCANACATCACACAACATAACACCTTACTCTNCTTTC :  60

                   *        80         *       100         *       120
TrMDHb : TCTCTNAACAAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTCGATTCCTTCCATTTCT : 120

                   *       140         *       160         *       180
TrMDHb : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 180

                   *       200         *       220         *       240
TrMDHb : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 240

                   *       260         *       280         *       300
TrMDHb : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 300

                   *       320         *       340         *       360
TrMDHb : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 360

                   *       380         *       400         *       420
TrMDHb : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 420

                   *       440         *       460         *       480
TrMDHb : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 480

                   *       500         *       520         *       540
TrMDHb : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 540

                   *       560         *       580         *       600
TrMDHb : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 600

                   *       620         *       640         *       660
TrMDHb : CTTGATCACAACAGGGCATTGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 660

                   *       680         *       700         *       720
TrMDHb : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 720

                   *       740         *       760         *       780
TrMDHb : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC : 780

                   *       800         *       820         *       840
TrMDHb : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT : 840

                   *       860         *       880         *       900
TrMDHb : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 900

                   *       920         *       940         *       960
TrMDHb : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 960
```

```
                 *       980          *       1000          *       1020
TrMDHb : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 1020

                 *      1040          *       1060          *       1080
TrMDHb : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

                 *      1100          *
TrMDHb : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 1111
```

re 59 Deduced amino acid sequence of TrMDHb

```
                    *        20         *        40         *        60
TrMDHb : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD :  60

                    *        80         *       100         *       120
TrMDHb : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEKH : 120

                    *       140         *       160         *       180
TrMDHb : AAANCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLNVQVSDVK : 180

                    *       200         *       220         *       240
TrMDHb : NVIIWGNHSSTQYPDVNHATVNTPAGEKPVRELVSDDAWLNGEFISTVQQRGAAIIKARK : 240

                    *       260         *       280         *       300
TrMDHb : LSSALSAASAACDHIRDWVLGTPQGTFVSMGVYSDGSYNVPAGLIYSFPVTTANGEWKIV : 300

                    *       320
TrMDHb : QGLSIDEFSRKKLDLTAEELSEEKSLAY : 328
```

Figure 60 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHb

```
             .       *        20         *        40         *        60
TrMDHb1  : TTCTCCCNNAATCNNGAAANC-NCGC-ACA-CA-ACA-C-TAA-ACT--ACT-A-C-T-C : 47
TrMDHb2  : TTCTCNCANAATCNNGAAANC-CCGC-A-A--A-ACA-C-TAA-ACT--ACT-A-C-T-C : 45
TrMDHb3  : -----------GNNACCACAA-CACA-ACA-CA-NCA-C-TAA-GCCT--CACT-C--TC : 37
TrMDHb4  : ------------------GTT-NTCA-ACA-CA-ACA-C-TCAC-CCTTNCTNN-C-T-C : 32
TrMDHb5  : ---------------------GCNCANACATAACACAACACTAAACCT-NA-CT--NCTC : 35
TrMDHb6  : ----------------------GCAA-ACA-CA-ACA-C-TAA-GCT-NACT-N-C--TC : 27
TrMDHb7  : -----------------------TTT-ACC-TA-ACC-C-TAN-ACTCCACT-N-C-TTC : 28
TrMDHb8  : -----------------------------C-NA-CCACC-TAAC-CCTGACTNN-C-TNC : 25
TrMDHb9  : -----------------------------------CN-A-NCC-TC---ACT-A-C-TNC : 16
TrMDHb10 : -----------------------------------CANCACTAAACC--TA-CT-CNCAC : 21
TrMDHb11 : ------------------------------------CAAACA-CACCT-AACCTAC-TNC : 21
TrMDHb12 : ------------------------------------AACACTAAACCC-TA-CTNCTCTC : 22
TrMDHb13 : -------------------------------------CN-TAAC-CCTNACTCN-C-T-C : 18
TrMDHb14 : --------------------------------------C-TCA-TC---ACT-N-C-TNC : 14
TrMDHb15 : --------------------------------------CACTAAACCT-NN-CTNCTCTC : 20
TrMDHb16 : ---------------------------------------CNACCACNTAAAACTNC-TNC : 20
TrMDHb17 : -----------------------------------------ACCACNTAACCCT-CCTNC : 18
TrMDHb18 : -----------------------------------------A-CACNT-AACCTNC-TNC : 16
TrMDHb19 : -----------------------------------------------CTANCCT-CACTC : 12
TrMDHb20 : -------------------------------------------------GCA-T-C--TC :  7
TrMDHb21 : --------------------------------------------------------TCAC :  4
TrMDHb22 : ----------------------------------------------------------TC :  2
TrMDHb23 : ------------------------------------------------------------ :  -
TrMDHb24 : ------------------------------------------------------------ :  -
TrMDHb25 : ------------------------------------------------------------ :  -
TrMDHb26 : ------------------------------------------------------------ :  -
TrMDHb27 : ------------------------------------------------------------ :  -
TrMDHb28 : ------------------------------------------------------------ :  -
TrMDHb29 : ------------------------------------------------------------ :  -
TrMDHb30 : ------------------------------------------------------------ :  -
TrMDHb31 : ------------------------------------------------------------ :  -
TrMDHb32 : ------------------------------------------------------------ :  -
```

```
                    *         80         *        100         *        120
TrMDHb1  : TCT---AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT : 104
TrMDHb2  : TCT---AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT : 102
TrMDHb3  : TNA---AACAAAAACTGTTCTTCCACTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  94
TrMDHb4  : TCT:NAAACAAANGCTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  91
TrMDHb5  : TCT-N-AA-NAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCC-GTTCT :  91
TrMDHb6  : TCT---NAACAAAACTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGGGTCT :  84
TrMDHb7  : TNN---AACAAAAACTATTCTTNATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  85
TrMDHb8  : TCT-NNAACAAAAACTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  84
TrMDHb9  : TCN---AACAAAAACTGTTCTTCC-CTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  72
TrMDHb10 : TCTCA-AAC-AAAACTGNTCTTCCTCTCTTAA-CTTCCCTGTTCGATTCCTTCCAGTTCT :  78
TrMDHb11 : TCTCTNAAC-AAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT :  80
TrMDHb12 : TCTCT-NAACAAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCCAGTTCT :  81
TrMDHb13 : TCT-N-AAANAAAACTATTCTT-ATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  75
TrMDHb14 : TNC---AANAAAAACTGTTCTTCCACTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  71
TrMDHb15 : TCTCT-AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTCGATTCCTTCCAGTTCT :  79
TrMDHb16 : TCTCTNAAC-AAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  78
TrMDHb17 : TCT-CAAACAAAAACTGTTCTTC-CCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  76
TrMDHb18 : TCTCTGAAC-AAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCC-GTTCT :  74
TrMDHb19 : TCT-NNAACAAAAACTGTTCTTC-CCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  70
TrMDHb20 : TNA---AACAAAAACTGTTCTT-CNCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  63
TrMDHb21 : CCTCTNAACAAAAACTGTTCTTCCTCCCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  63
TrMDHb22 : TCT--NAACAAAAACTGTTCTTC-CCTCTTNATCTTCCCTGTTCGATTCCTTCTATTTCT :  59
TrMDHb23 : --------CAAAAACTGGTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCC-GTTCT :  51
TrMDHb24 : ----------AAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCC-GTTCT :  49
TrMDHb25 : --------------GNNTTCTTCCTCTCTTGAACTTCCCTGTTTGATTCCTTCCAGTTCT :  46
TrMDHb26 : ---------------GGTTCTTC-CCTCTTATNCTTCCCTGTTCGATTCCTTCTATTTCT :  44
TrMDHb27 : --------------------TTCCTCTCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  39
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
```

```
                        *        140         *        160         *        180
TrMDHb1  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 164
TrMDHb2  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 162
TrMDHb3  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 154
TrMDHb4  : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 151
TrMDHb5  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 151
TrMDHb6  : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 144
TrMDHb7  : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 145
TrMDHb8  : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 144
TrMDHb9  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 132
TrMDHb10 : TCAAAAATGGCCNAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCNGGGCAAATTGGT : 138
TrMDHb11 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 140
TrMDHb12 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 141
TrMDHb13 : TCAGCAATGGCCAAAGACCCAGTTCGTTTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 135
TrMDHb14 : TCAAAAATGGCCAAANACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 131
TrMDHb15 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 139
TrMDHb16 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 138
TrMDHb17 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 136
TrMDHb18 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 134
TrMDHb19 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 130
TrMDHb20 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 123
TrMDHb21 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 123
TrMDHb22 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 119
TrMDHb23 : T-NAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 110
TrMDHb24 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 109
TrMDHb25 : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 106
TrMDHb26 : T-NAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 103
TrMDHb27 : TC-AAAATGGCC-AAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT :  97
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
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                   *       200         *       220         *       240
TrMDHb1  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 224
TrMDHb2  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 222
TrMDHb3  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 214
TrMDHb4  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb5  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb6  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb7  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205
TrMDHb8  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb9  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192
TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200
TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201
TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195
TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191
TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199
TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196
TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194
TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190
TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179
TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170
TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169
TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166
TrMDHb26 : TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163
TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157
TrMDHb28 : -------------------------GGGGAGTGATGCTTGGTCCTGAT-NACCTGTGATC :  34
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
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                         *       260         *       280         *       300
TrMDHb1   : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGATG : 284
TrMDHb2   : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 282
TrMDHb3   : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 274
TrMDHb4   : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 271
TrMDHb5   : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 271
TrMDHb6   : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGNCATTGAATGGAGTTAAAATGGAGTTG : 264
TrMDHb7   : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 265
TrMDHb8   : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 264
TrMDHb9   : CTTGACATGCTTGATATTGCTGCAGNAGNAGAGTNATTGAATGGAGCTAAAATGGAGCTG : 252
TrMDHb10  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 258
TrMDHb11  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 260
TrMDHb12  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 261
TrMDHb13  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 255
TrMDHb14  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 251
TrMDHb15  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 259
TrMDHb16  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 258
TrMDHb17  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 256
TrMDHb18  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 254
TrMDHb19  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 250
TrMDHb20  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 243
TrMDHb21  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 243
TrMDHb22  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 239
TrMDHb23  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 230
TrMDHb24  : CTACACATGCTTGATATTCCACCCGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 229
TrMDHb25  : CTTCACATGCTTGATATTCCTACAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 226
TrMDHb26  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 223
TrMDHb27  : CTTCACATGCTTGATATTCTTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 217
TrMDHb28  : CTT-NCATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG :  93
TrMDHb29  : -------------NTATTCCTNCNGCAGCNGAGT-NTTGAATGGAG-TAAGATGGAGTTG :  45
TrMDHb30  : --------------TATTCCT-CCGCAGCAGAGT-NTTGAATGGAG-TAAGATGGAGTTG :  43
TrMDHb31  : ------------------------------------------------------------ :   -
TrMDHb32  : ------------------------------------------------------------ :   -
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                      *        320         *        340         *        360
TrMDHb1  : GNCGATGCTGNATTNNCACTTGTTAAAGGNGANGCTGCT--------------------- : 323
TrMDHb2  : GTCGATGCTGCATTTCCACTTGTTAAAGGTGNTGATGNTACAACTGATGATGCNGAGCNA : 342
TrMDHb3  : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 334
TrMDHb4  : GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA : 331
TrMDHb5  : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 331
TrMDHb6  : GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA : 324
TrMDHb7  : GCGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA : 325
TrMDHb8  : GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA : 324
TrMDHb9  : CCGGATGCTGNATTNNAACTTCTTACAGGCGCCGCCGCTACCACTGATGGTGCCCAACCA : 312
TrMDHb10 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 318
TrMDHb11 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 320
TrMDHb12 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 321
TrMDHb13 : GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA : 315
TrMDHb14 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 311
TrMDHb15 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 319
TrMDHb16 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 318
TrMDHb17 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 316
TrMDHb18 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 314
TrMDHb19 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 310
TrMDHb20 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 303
TrMDHb21 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 303
TrMDHb22 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 299
TrMDHb23 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 290
TrMDHb24 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 289
TrMDHb25 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 286
TrMDHb26 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 283
TrMDHb27 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 277
TrMDHb28 : GTGGATGCTGCATTTCCACTTCTTAAAGGCATTGTTGCTACAACTGATGTTGTTGAAGCA : 153
TrMDHb29 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 105
TrMDHb30 : GTCGATGCTGCATTTCC-CTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 102
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
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		* 380 * 400 * 420		
TrMDHb1	:	---	:	-
TrMDHb2	:	TNNNCTGG---	:	350
TrMDHb3	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	394
TrMDHb4	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	391
TrMDHb5	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	391
TrMDHb6	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	384
TrMDHb7	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	385
TrMDHb8	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	384
TrMDHb9	:	TGCGCTGCA-CCGATATNGCNN---------------------------------------	:	333
TrMDHb10	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAN	:	378
TrMDHb11	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	380
TrMDHb12	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	381
TrMDHb13	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	375
TrMDHb14	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	371
TrMDHb15	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	379
TrMDHb16	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	378
TrMDHb17	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	376
TrMDHb18	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	374
TrMDHb19	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	370
TrMDHb20	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTNTGGAG	:	363
TrMDHb21	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	363
TrMDHb22	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	359
TrMDHb23	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	350
TrMDHb24	:	TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	349
TrMDHb25	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	346
TrMDHb26	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	343
TrMDHb27	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	337
TrMDHb28	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	213
TrMDHb29	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	165
TrMDHb30	:	TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	162
TrMDHb31	:	--GGAG	:	4
TrMDHb32	:	--NNNN	:	4

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                  *        440         *         460         *        480
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 454
TrMDHb4  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 451
TrMDHb5  : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 451
TrMDHb6  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 444
TrMDHb7  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCAGCCCTTGAA : 445
TrMDHb8  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 444
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 438
TrMDHb11 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 440
TrMDHb12 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 441
TrMDHb13 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 435
TrMDHb14 : AGGAAGGATGTGATGACTAANAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 431
TrMDHb15 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 439
TrMDHb16 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 438
TrMDHb17 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 436
TrMDHb18 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 434
TrMDHb19 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 430
TrMDHb20 : AGGAAGGATGTGATGACTAAGANTGTCTCTATTTACAANANNNAGNCTTNTGNCCTTGAA : 423
TrMDHb21 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 423
TrMDHb22 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 419
TrMDHb23 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 410
TrMDHb24 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 409
TrMDHb25 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 406
TrMDHb26 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 403
TrMDHb27 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 397
TrMDHb28 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 273
TrMDHb29 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 225
TrMDHb30 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 222
TrMDHb31 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA :  64
TrMDHb32 : NNGNANGNNGTGATGTCTAANAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA :  64
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                    *        500         *        520         *        540
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 514
TrMDHb4  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 511
TrMDHb5  : AAGCATGCTGCTGCCAACTGCAAGGNTTTGGTTGNTGCTAACCCANC-AACACCAATGCA : 510
TrMDHb6  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 504
TrMDHb7  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 505
TrMDHb8  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 504
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 498
TrMDHb11 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA : 499
TrMDHb12 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 501
TrMDHb13 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 495
TrMDHb14 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGG----------------------------- : 462
TrMDHb15 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 499
TrMDHb16 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 498
TrMDHb17 : AAGCATGCTGCTGCCAACTGCAAGGNTTTGGGTATTGCTAACCCANCAAATACCAATGCA : 496
TrMDHb18 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA : 493
TrMDHb19 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 490
TrMDHb20 : AAAGATNCTG-------------------------------------------------- : 433
TrMDHb21 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 483
TrMDHb22 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 479
TrMDHb23 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 470
TrMDHb24 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 469
TrMDHb25 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 466
TrMDHb26 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 463
TrMDHb27 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 457
TrMDHb28 : AAGCAAGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 333
TrMDHb29 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 285
TrMDHb30 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 282
TrMDHb31 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 124
TrMDHb32 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 124
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                         *        560         *        580         *        600
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 574
TrMDHb4  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 571
TrMDHb5  : TTGATCTTGNAGGAATCNGCT--------------------------------------- : 531
TrMDHb6  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 564
TrMDHb7  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 565
TrMDHb8  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 564
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTNGACTAGA : 558
TrMDHb11 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 559
TrMDHb12 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 561
TrMDHb13 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 555
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 559
TrMDHb16 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 558
TrMDHb17 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGANAAAAACATTTCANGTTTG------ : 550
TrMDHb18 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 553
TrMDHb19 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 550
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 543
TrMDHb22 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 539
TrMDHb23 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 530
TrMDHb24 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 529
TrMDHb25 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 526
TrMDHb26 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 523
TrMDHb27 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 517
TrMDHb28 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGCTTTGACTAGA : 393
TrMDHb29 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 345
TrMDHb30 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 342
TrMDHb31 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 184
TrMDHb32 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 184
```

```
                   *        620         *        640         *        660
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : CTTGATCACAA------------------------------------------------- : 585
TrMDHb4  : CTTGATCACAACAGGGCATTGG-------------------------------------- : 593
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : CTTGATCAC--------------------------------------------------- : 573
TrMDHb7  : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 603
TrMDHb8  : CTTGATCACAACAGGGCATTGGGCCAAATTTCT--------------------------- : 597
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : CTTGATCAC--------------------------------------------------- : 567
TrMDHb11 : CTTGATCACC-------------------------------------------------- : 569
TrMDHb12 : CTTGATCACAACAGGGCATTGGGCCAAATTT----------------------------- : 592
TrMDHb13 : CTTGATCACAACAGGGCATTGGGCCAAATT------------------------------ : 585
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : CTTGATCACAACAG---------------------------------------------- : 573
TrMDHb16 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAAT--------------- : 603
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 591
TrMDHb19 : CTTGATCACAACAGGGCATTG--------------------------------------- : 571
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTG------------------ : 585
TrMDHb22 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 599
TrMDHb23 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 568
TrMDHb24 : CTTGATCACAACAGGGCATTGGGCCAAAT------------------------------- : 558
TrMDHb25 : CCTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 586
TrMDHb26 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 583
TrMDHb27 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTC---- : 573
TrMDHb28 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 453
TrMDHb29 : CTTGATCACAACAGGGCATTGNGCCAAATTTCTGAAAGATTGAATGTCCAAGTTTCTGAT : 405
TrMDHb30 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTCCAAGTTTCTGAT : 402
TrMDHb31 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 244
TrMDHb32 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 244
```

```
                    *       680         *       700         *       720
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : GTAAAGAATGT------------------------------------------------- : 610
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 646
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 513
TrMDHb29 : GTAAAGAATGTCATTATCTGGNGTAATCATTCATCAACTCAGCATCCTGATGTCAACCAT : 465
TrMDHb30 : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 462
TrMDHb31 : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 304
TrMDHb32 : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 304
```

```
                    *        740         *        760         *        780
TrMDHb1   : ------------------------------------------------------------ :    -
TrMDHb2   : ------------------------------------------------------------ :    -
TrMDHb3   : ------------------------------------------------------------ :    -
TrMDHb4   : ------------------------------------------------------------ :    -
TrMDHb5   : ------------------------------------------------------------ :    -
TrMDHb6   : ------------------------------------------------------------ :    -
TrMDHb7   : ------------------------------------------------------------ :    -
TrMDHb8   : ------------------------------------------------------------ :    -
TrMDHb9   : ------------------------------------------------------------ :    -
TrMDHb10  : ------------------------------------------------------------ :    -
TrMDHb11  : ------------------------------------------------------------ :    -
TrMDHb12  : ------------------------------------------------------------ :    -
TrMDHb13  : ------------------------------------------------------------ :    -
TrMDHb14  : ------------------------------------------------------------ :    -
TrMDHb15  : ------------------------------------------------------------ :    -
TrMDHb16  : ------------------------------------------------------------ :    -
TrMDHb17  : ------------------------------------------------------------ :    -
TrMDHb18  : ------------------------------------------------------------ :    -
TrMDHb19  : ------------------------------------------------------------ :    -
TrMDHb20  : ------------------------------------------------------------ :    -
TrMDHb21  : ------------------------------------------------------------ :    -
TrMDHb22  : ------------------------------------------------------------ :    -
TrMDHb23  : ------------------------------------------------------------ :    -
TrMDHb24  : ------------------------------------------------------------ :    -
TrMDHb25  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC :  706
TrMDHb26  : ------------------------------------------------------------ :    -
TrMDHb27  : ------------------------------------------------------------ :    -
TrMDHb28  : GCAACTGTTAACACCCCCGCCGGGGAGAAGCCTGTCCGTGAACTTGTTT----------- :  562
TrMDHb29  : GCAACTGTTAACACCCNCGCTGNNGAGAAGCCTGNCCGTGAGCTNGTTTC---------- :  515
TrMDHb30  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC :  522
TrMDHb31  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC :  364
TrMDHb32  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC :  364
```

```
                    *        800         *        820         *        840
TrMDHb1  : ------------------------------------------------------------ :    -
TrMDHb2  : ------------------------------------------------------------ :    -
TrMDHb3  : ------------------------------------------------------------ :    -
TrMDHb4  : ------------------------------------------------------------ :    -
TrMDHb5  : ------------------------------------------------------------ :    -
TrMDHb6  : ------------------------------------------------------------ :    -
TrMDHb7  : ------------------------------------------------------------ :    -
TrMDHb8  : ------------------------------------------------------------ :    -
TrMDHb9  : ------------------------------------------------------------ :    -
TrMDHb10 : ------------------------------------------------------------ :    -
TrMDHb11 : ------------------------------------------------------------ :    -
TrMDHb12 : ------------------------------------------------------------ :    -
TrMDHb13 : ------------------------------------------------------------ :    -
TrMDHb14 : ------------------------------------------------------------ :    -
TrMDHb15 : ------------------------------------------------------------ :    -
TrMDHb16 : ------------------------------------------------------------ :    -
TrMDHb17 : ------------------------------------------------------------ :    -
TrMDHb18 : ------------------------------------------------------------ :    -
TrMDHb19 : ------------------------------------------------------------ :    -
TrMDHb20 : ------------------------------------------------------------ :    -
TrMDHb21 : ------------------------------------------------------------ :    -
TrMDHb22 : ------------------------------------------------------------ :    -
TrMDHb23 : ------------------------------------------------------------ :    -
TrMDHb24 : ------------------------------------------------------------ :    -
TrMDHb25 : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTG-------------- :  752
TrMDHb26 : ------------------------------------------------------------ :    -
TrMDHb27 : ------------------------------------------------------------ :    -
TrMDHb28 : ------------------------------------------------------------ :    -
TrMDHb29 : ------------------------------------------------------------ :    -
TrMDHb30 : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT :  582
TrMDHb31 : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT :  424
TrMDHb32 : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT :  424
```

```
                    *        860         *        880         *        900
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : AGAAAGCTTTCAAGEG-------------------------------------------- : 598
TrMDHb31 : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 484
TrMDHb32 : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 484
```

```
                     *         920         *         940         *         960
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 544
TrMDHb32 : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 544
```

```
                           *        980         *        1000         *        1020
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAA- : 603
TrMDHb32 : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 604
```

```
                        *       1040         *       1060         *       1080
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 664
```

```
                          *        1100        *
TrMDHb1   : ------------------------------- :   -
TrMDHb2   : ------------------------------- :   -
TrMDHb3   : ------------------------------- :   -
TrMDHb4   : ------------------------------- :   -
TrMDHb5   : ------------------------------- :   -
TrMDHb6   : ------------------------------- :   -
TrMDHb7   : ------------------------------- :   -
TrMDHb8   : ------------------------------- :   -
TrMDHb9   : ------------------------------- :   -
TrMDHb10  : ------------------------------- :   -
TrMDHb11  : ------------------------------- :   -
TrMDHb12  : ------------------------------- :   -
TrMDHb13  : ------------------------------- :   -
TrMDHb14  : ------------------------------- :   -
TrMDHb15  : ------------------------------- :   -
TrMDHb16  : ------------------------------- :   -
TrMDHb17  : ------------------------------- :   -
TrMDHb18  : ------------------------------- :   -
TrMDHb19  : ------------------------------- :   -
TrMDHb20  : ------------------------------- :   -
TrMDHb21  : ------------------------------- :   -
TrMDHb22  : ------------------------------- :   -
TrMDHb23  : ------------------------------- :   -
TrMDHb24  : ------------------------------- :   -
TrMDHb25  : ------------------------------- :   -
TrMDHb26  : ------------------------------- :   -
TrMDHb27  : ------------------------------- :   -
TrMDHb28  : ------------------------------- :   -
TrMDHb29  : ------------------------------- :   -
TrMDHb30  : ------------------------------- :   -
TrMDHb31  : ------------------------------- :   -
TrMDHb32  : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 695
```

Figure 61   Consensus contig nucleotide sequence of TrMDHc

```
                   *        20         *        40         *        60
TrMDHc : AAAGNGAATTGGAATATACGACACTCCATTCCATACTTCCATTCCNTACTTTGCTTTCTC :  60

                   *        80         *       100         *       120
TrMDHc : GCTCTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGG : 120

                   *       140         *       160         *       180
TrMDHc : CCGTCGATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGC : 180

                   *       200         *       220         *       240
TrMDHc : CGTGGCTATGCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGC : 240

                   *       260         *       280         *       300
TrMDHc : GGGATCGGCCAGCCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCT : 300

                   *       320         *       340         *       360
TrMDHc : CTTTATGATATTGCTGGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGA : 360

                   *       380         *       400         *       420
TrMDHc : TCTGAGGTAACTGGGTATGCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGAT : 420

                   *       440         *       460         *       480
TrMDHc : GTTGTTATAATTCCTGCTGGTGTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTC : 480

                   *       500         *       520         *       540
TrMDHc : AATATTAACGCTGGCATTGTCAAGTCACTTGCCACTGCTATTTCTAAGTACTGCCCCCAT : 540

                   *       560         *       580         *       600
TrMDHc : GCCCTTGTTAACATGATAAGCAACCCTGTGAACTCCACCGTTCCCATTGCTGCAGAGGTT : 600

                   *       620         *       640         *       660
TrMDHc : TTCAAGAAGGCAGGGACATATGACGAGAAGAGATTGTTTGGGGTTACAACCCTTGATGTA : 660

                   *       680         *       700         *       720
TrMDHc : GTCAGGGCAAAAACTTTCTATGCCGGGAAAGCTAAAGTTCCAGTTGCCGAGGTCAATGTA : 720

                   *       740         *       760         *       780
TrMDHc : CCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTTCCATTATTTTNTCAGGCAACACCT : 780

                   *       800         *       820         *       840
TrMDHc : CAAGCCAATCTGGGTGATGATACCCTTAAGGNTTTAACGGNANGGACACAAGATGGAGGA : 840

                   *       860         *       880         *       900
TrMDHc : ACAGAAGTTGNGACCGCCAAGGCTGGAAAGGGTTCTGCAACTTTGTCAATGGCTTATGCT : 900

                   *       920         *       940         *       960
TrMDHc : GGAGCCATATTTGCTGATGCTNGCCTCAAAGGNCTGAATGGAGTTCCAGATGTTATTGAG : 960
```

```
                   *       980          *       1000          *       1020
TrMDHc : TGCTCATATGTGCAATCCAATATCATCTCTGACCTTCCTTTCTTTGCTTCCAAGGTGAGG : 1020

                   *      1040          *       1060          *       1080
TrMDHc : ATTGGGAAGAATGGTGTGGAAGAAATTCTGGCTTAGGTTCTCTCACAGATTTCGAGCAA : 1080

                   *      1100          *       1120          *       1140
TrMDHc : CAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATCAAATTT : 1140

                   *      1160          *       1180          *       1200
TrMDHc : GCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTTCCATTTAGAACCAGATCAA : 1200

                   *      1220          *       1240          *       1260
TrMDHc : ATTTTGCAAATTCAGAACAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTTAA : 1260

                   *      1280          *       1300          *       1320
TrMDHc : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTTAGG : 1320

                   *      1340          *       1360          *       1380
TrMDHc : TTGGCCTTTCCATTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAA : 1380

                   *      1400
TrMDHc : GGGTGNTGGNCANCGATACACANCCCCC : 1408
```

Figure 62 Deduced amino acid sequence of TrMDHc

```
                  *        20         *        40         *        60
TrMDHc : MRPSMLRSVQSAVSRASSHLTRRGYATEPVPERKVAILGAAGGIGQPLSLLMKLNPLVST :  60

                  *        80         *       100         *       120
TrMDHc : LSLYDIAGTPGVAADVSHINSRSEVTGYAGEEELGKALEGADVVIIPAGVPRKPGMTRDD : 120

                  *       140         *       160         *       180
TrMDHc : LFNINAGIVKSLATAISKYCPHALVNMISNPVNSTVPIAAEVFKKAGTYDEKRLFGVTTL : 180

                  *       200         *       220         *       240
TrMDHc : DVVRAKTFYAGKAKVPVAEVNVPVIGGHAGVTILPLFXQATPQANLGDDTLKXLTXXTQD : 240

                  *       260         *       280         *       300
TrMDHc : GGTEVXTAKAGKGSATLSMAYAGAIFADAXLKXLNGVPDVIECSYVQSNIISDLPFFASK : 300

                  *       320         *       340
TrMDHc : VRIGKNGVEEILGLGSLTDFEQQGLENLKAELKSSIEKGIKFASQ : 345
```

Figure 63 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHc

```
                         *        20         *        40         *        60
TrMDHc1  : AAAGNGAATTGGAATNT-CGAC-CTCCATTCCNTACT-TTATTTCATTCATCGCTCTCTTCT :  60
TrMDHc2  : ---GTTTNATTGGAATATACNGCACTCCATTCCATACT-TTATTTCATTCATCGCTCTCTTCT :  59
TrMDHc3  : -------------------GNNCATCGA-CACTCGCTTCCCTACTTTGCTTT-NTTTATCGCT :  42
TrMDHc4  : ------------------------------GNACT-CCATTCCNTACTTTNTTTNTTNTCG :  30
TrMDHc5  : ---------------------------------GCATCC-TTCCNTACTTT-NTTCNTCGCT :  27
TrMDHc6  : ----------------------------------CNTCCATGCCNTACTTT-NTTCNTCGCT :  27
TrMDHc7  : ----------------------------------GNTTCGTTCCCTACTTT-CATTCCATCG :  27
TrMDHc8  : ------------------------------------TGCCATTCCNTACTTTNTTTATTNTCG :  27
TrMDHc9  : -------------------------------------TCCATTCCNTACTCT-ATTTNTCGCT :  25
TrMDHc10 : -------------------------------------TCC-TTCCATACTTTGATTCATCGCT :  25
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                *        80         *        100        *        120
TrMDHc1  : CTCTCTCTCTTTATTCTCGAAAAGCTTGTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG : 122
TrMDHc2  : CTCTCTCT-T-TATTCTCGAAAAGCTTTTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG : 119
TrMDHc3  : CTCTCTCTTTTTATTCTCGAAAAGCTTTTTCAGCCATCAACGGAGAGAATTATGAGTCCGTCG : 105
TrMDHc4  : CTCTCTCTCTGTATTCTCGAAAAGCTTTTTCAGCC-ACAACG-AGAGAATAATGAGGCCGTCG :  91
TrMDHc5  : CTCTCTC--TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  88
TrMDHc6  : CTCTCTC--TTTATTCTCGAAAAGCTTTTT-AGCCAACAACGGAGAGAATTATGAGGCCGTCG :  87
TrMDHc7  : CTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  90
TrMDHc8  : CTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG :  89
TrMDHc9  : CTCTCTCTTTATATTCTCGAAAAGCTTTTT-NGCCATCAACGGAGAGAATTATGAGGCCGTCG :  87
TrMDHc10 : CTCTCTC--TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  86
TrMDHc11 : -----------GNNTCTCG-AAAGCTTTTT-NGCC--TAACGGAGAGAATTATGAGGCCGTCG :  48
TrMDHc12 : -------------TTCTCAAAAAGCTTTTT-AGCC-ACAACG-AGAGAA-AATGAGGCCGTCG :  46
TrMDHc13 : -------------TTCTCG-AAAGCTTTTTCAGCC-ACAACGNANAGAATAATGAGGCCGTCG :  48
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

              *       140         *        160         *        180
TrMDHc1  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 185
TrMDHc2  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 182
TrMDHc3  : ATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 168
TrMDHc4  : ATGCTCAGATCTGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 154
TrMDHc5  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 151
TrMDHc6  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 150
TrMDHc7  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 153
TrMDHc8  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 152
TrMDHc9  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 150
TrMDHc10 : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 149
TrMDHc11 : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 111
TrMDHc12 : ATGCTCAGATCTGTCC-ATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGGTAT : 108
TrMDHc13 : ATGCTCAGATCTGTCCAATCAGCCGTATCCCGGGCCTCGTCTCACCTAACCCGCCGTGGGTAT : 111
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -
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                 *        200         *        220         *        240         *
TrMDHc1  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 248
TrMDHc2  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 245
TrMDHc3  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 231
TrMDHc4  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 217
TrMDHc5  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 214
TrMDHc6  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 213
TrMDHc7  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 216
TrMDHc8  : GCTACCGAACCAGTTCCAGAACGCAGGGTGGCCATTCTCGGTGCTGCTGGCGGGATCGGACAG : 215
TrMDHc9  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 213
TrMDHc10 : GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 212
TrMDHc11 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 174
TrMDHc12 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCTGGCGGGATCGGCCAG : 171
TrMDHc13 : GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 174
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

             260         *        280         *        300         *
TrMDHc1  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 311
TrMDHc2  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 308
TrMDHc3  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 294
TrMDHc4  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 280
TrMDHc5  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 277
TrMDHc6  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 276
TrMDHc7  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 279
TrMDHc8  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 278
TrMDHc9  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 276
TrMDHc10 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 275
TrMDHc11 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 237
TrMDHc12 : CCTCTCTCTCTTCTCATGAAGCTCAATCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 234
TrMDHc13 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 237
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

          320         *        340         *        360         *        3
TrMDHc1  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 374
TrMDHc2  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 371
TrMDHc3  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 357
TrMDHc4  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 343
TrMDHc5  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 340
TrMDHc6  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 339
TrMDHc7  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 342
TrMDHc8  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 341
TrMDHc9  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 339
TrMDHc10 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 338
TrMDHc11 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 300
TrMDHc12 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 297
TrMDHc13 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 300
TrMDHc14 : --------GNGTGTCGCCGCTGNNGTCAGCCACATCAACTCCANANCTGA-GTAACTGGGTAT :  54
TrMDHc15 : -----------------GNTGATGT-NGCC-CAT-AACTCC-GATCTGAGGTAACTGGGTAT :  41
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -
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              80       *       400       *       420       *       440
TrMDHc1  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 437
TrMDHc2  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 434
TrMDHc3  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 420
TrMDHc4  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 406
TrMDHc5  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 403
TrMDHc6  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 402
TrMDHc7  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 405
TrMDHc8  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 404
TrMDHc9  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 402
TrMDHc10 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 401
TrMDHc11 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 363
TrMDHc12 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 360
TrMDHc13 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 363
TrMDHc14 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 117
TrMDHc15 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 104
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                  *       460       *       480       *       500
TrMDHc1  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 500
TrMDHc2  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 497
TrMDHc3  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTTAATATTAATGCTGGCATTGTCAAG : 483
TrMDHc4  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 469
TrMDHc5  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 466
TrMDHc6  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 465
TrMDHc7  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 468
TrMDHc8  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 467
TrMDHc9  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTTAAG : 465
TrMDHc10 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 464
TrMDHc11 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 426
TrMDHc12 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 423
TrMDHc13 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 426
TrMDHc14 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 180
TrMDHc15 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 167
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

               *       520       *       540       *       560
TrMDHc1  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATG-------------------------- : 537
TrMDHc2  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 560
TrMDHc3  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 546
TrMDHc4  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 532
TrMDHc5  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 529
TrMDHc6  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 528
TrMDHc7  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 531
TrMDHc8  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 530
TrMDHc9  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 528
TrMDHc10 : TCACTTGCCACTGGTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 527
TrMDHc11 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 489
TrMDHc12 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 486
TrMDHc13 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 489
TrMDHc14 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 243
TrMDHc15 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 230
TrMDHc16 : --------------------------------------------------------TTG---- :   3
TrMDHc17 : --------------------------------------------------------------- :   -
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                  *     580         *       600         *       620         *
TrMDHc1   : ---------------------------------------------------------------- :   -
TrMDHc2   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGG---------------- : 608
TrMDHc3   : GTGAACTCCACCGTTCCCATTGCTGCAGG----------------------------------- : 575
TrMDHc4   : GTGAACTCCACCGTTCCCATTGCTGCAGAGG--------------------------------- : 563
TrMDHc5   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATAT---------- : 583
TrMDHc6   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 591
TrMDHc7   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 594
TrMDHc8   : GTGAACTCCACCGTTCCCATTGCTGC-------------------------------------- : 556
TrMDHc9   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 591
TrMDHc10  : GTGAACTCCACCGTTCCCATTGCTGNAGAGGTTTTCAAGAAGGCNGGGACATATGACNAGAAN : 590
TrMDHc11  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 552
TrMDHc12  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 549
TrMDHc13  : GTGAACTCCACCGTTCCCATTGCTGCANAGGTTTTCAAGAAGGCAGGGACATATGACNAGAAG : 552
TrMDHc14  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 306
TrMDHc15  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 293
TrMDHc16  : ---------------------------------------------------------------- :   -
TrMDHc17  : ---------------------------------------------------------------- :   -

                 640         *       660         *       680         *
TrMDHc1   : ---------------------------------------------------------------- :   -
TrMDHc2   : ---------------------------------------------------------------- :   -
TrMDHc3   : ---------------------------------------------------------------- :   -
TrMDHc4   : ---------------------------------------------------------------- :   -
TrMDHc5   : ---------------------------------------------------------------- :   -
TrMDHc6   : AGATTGT--------------------------------------------------------- : 598
TrMDHc7   : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACTTTTTATGCCGGGAAAGCT : 657
TrMDHc8   : ---------------------------------------------------------------- :   -
TrMDHc9   : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACTTTCTATGCCGGGAAAGCT : 654
TrMDHc10  : ANATTGTTTGGGGTT-CAACCCTTGATGTAGTCAGGGGGAAAACTTTTTTTGCCGGGAAAGCT : 652
TrMDHc11  : AGATTGTTTGGGGTTACAACCCTTG--------------------------------------- : 577
TrMDHc12  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACT------------------- : 594
TrMDHc13  : AGATTGTTTGGGGTTACAACCCTTGATGTAGNCAGGGCAAAAACTTTTTATGCTGGGAAAGCT : 615
TrMDHc14  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACTTTCTATGCTGGGAAAGCT : 369
TrMDHc15  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACTTTCTATGCTGGGAAAGCT : 356
TrMDHc16  : ---------------------------------------------------------------- :   -
TrMDHc17  : ---------------------------------------------------------------- :   -

                .700         *       720         *       740         *
TrMDHc1   : ---------------------------------------------------------------- :   -
TrMDHc2   : ---------------------------------------------------------------- :   -
TrMDHc3   : ---------------------------------------------------------------- :   -
TrMDHc4   : ---------------------------------------------------------------- :   -
TrMDHc5   : ---------------------------------------------------------------- :   -
TrMDHc6   : ---------------------------------------------------------------- :   -
TrMDHc7   : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTTTTGGAGGCCATGCAGGAGTTACTATTNTT : 720
TrMDHc8   : ---------------------------------------------------------------- :   -
TrMDHc9   : AAAGTTCCAGTTGCCGAGGTCAATGTAC------------------------------------ : 682
TrMDHc10  : AAAGTTCCAGTTGCCGNGGGNAATGNNCCTGTTNTTGGAGGCC-TGC-NGAG-TNCTATT-NT : 711
TrMDHc11  : ---------------------------------------------------------------- :   -
TrMDHc12  : ---------------------------------------------------------------- :   -
TrMDHc13  : AAAGTTCCAGTTGCCGAGGNCAATGGACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTN : 678
TrMDHc14  : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTC : 432
TrMDHc15  : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTC : 419
TrMDHc16  : ---------------------------------------------------------------- :   -
TrMDHc17  : ---------------------------------------------------------------- :   -
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                   760         *        780         *        800         *       82
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : CCATTATTTTNTNAGG-AACACCTNAAGCCAATNTGGNTGATGAAACCCTTNAGGNTTTAACG : 782
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : CCGTTTTTTTATTAGG-CANNCCT-NANCCANT-TNGGNGATNAAA-CCTTAAGGGTTT-ACG : 769
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : CCATTATTTTNTNAGGCAACACCTNAAGCCAATNTGGGTGANGATNCCCTTAAGGNTTTAACG : 741
TrMDHc14 : CCATTATTTTCTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGCTCTAACG : 495
TrMDHc15 : CCATTATTTTCTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGCTCTAACG : 482
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

           0         *        840         *        860         *        880
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : GNANGGGCNCAAGATGGGGGAACNGAA-TTGNGACCGCCAAGGGTT----------------- : 827
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : GG-NNGGCNCAAAANG-GGGAACAAAA-NTTNGAC---------------------------- : 801
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : GNANGGACGCAANANGGAGGAACANAANTTNNGACCGCCANGG-TGG-AAGGGTTNT-NNACT : 801
TrMDHc14 : GGAAGGACACAAGATGGAGGAACAGAAGTTGTGACCGCCAAGGCTGGAAAGGGTTCTGCAACT : 558
TrMDHc15 : GCAAGGACACAAGATGGAGGAACAGAAGTTGTGACCGCCAAGGCTGGAAAGGGTTCTGCAACT : 545
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                 *        900         *        920         *        940
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : TT-NNAATGGN---------------------------------------------------- : 811
TrMDHc14 : TTGTCAATGGCTTATGCTGGAGCCATATTTGCTGATGCTTGCCTCAAAGGTCTGAATGGAGTT : 621
TrMDHc15 : TTGTCAATGGCT--------------------------------------------------- : 557
TrMDHc16 : -------------------------------CTGNTGCTNGCCT-NANGGNCTGAATGGAGTT :  34
TrMDHc17 : --------------------------------------------------------GNGNGTT :   7
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```
                 *       960         *       980         *      1000
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : CCAGATGTTATTGAGTGCTCATATGTGCAATCCAATATCATCTCTGACCTTNCTTTCTTTGCT : 684
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : -CNGANGTTATTGAACTCTCATATGTGCAATCCAATATCATCTNTGACCTTCCTTTCTTTGCT :  96
TrMDHc17 : CCAGATGTTATNGAGTGCT-NTATGTGC-AT-CNATAT-NTCTCTGACCTTCCTTTCTTTGCT :  66

             *       1020        *       1040        *       1060        *
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : TCCAAGGTGAGGATTGGGAANAATGGTGTGGGAANAAT------------------------- : 722
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : TCCAAGGNNNGGATTGGGAAGAATGGTGTGGAAGAGATTCTG--------------------- : 138
TrMDHc17 : TCC-AGGTGAGGATTGGGAAGAATGGTGTGGAAGAAATTCTGGGCTTAGGTTCTCTCACAGAT : 128

                 1080        *       1100        *       1120        *
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : TTCGAGCAACAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATC : 191
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                1140         *        1160         *        1180         *        1
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : AAATTTGCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTTCCATTTAGAACCAGAT : 254

            200          *        1220         *        1240         *        1260
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : CAAATTTTGCAAATTCAGAACAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTTAA : 317

                         *        1280         *        1300         *        1320
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTTAGGTTG : 380
```

```
                      *         1340          *         1360          *         1380
TrMDHc1  : -------------------------------------------------------------- :   -
TrMDHc2  : -------------------------------------------------------------- :   -
TrMDHc3  : -------------------------------------------------------------- :   -
TrMDHc4  : -------------------------------------------------------------- :   -
TrMDHc5  : -------------------------------------------------------------- :   -
TrMDHc6  : -------------------------------------------------------------- :   -
TrMDHc7  : -------------------------------------------------------------- :   -
TrMDHc8  : -------------------------------------------------------------- :   -
TrMDHc9  : -------------------------------------------------------------- :   -
TrMDHc10 : -------------------------------------------------------------- :   -
TrMDHc11 : -------------------------------------------------------------- :   -
TrMDHc12 : -------------------------------------------------------------- :   -
TrMDHc13 : -------------------------------------------------------------- :   -
TrMDHc14 : -------------------------------------------------------------- :   -
TrMDHc15 : -------------------------------------------------------------- :   -
TrMDHc16 : -------------------------------------------------------------- :   -
TrMDHc17 : GCCTTTCCATTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAAGGTGN : 443

                 *         1400
TrMDHc1  : ---------------------- :   -
TrMDHc2  : ---------------------- :   -
TrMDHc3  : ---------------------- :   -
TrMDHc4  : ---------------------- :   -
TrMDHc5  : ---------------------- :   -
TrMDHc6  : ---------------------- :   -
TrMDHc7  : ---------------------- :   -
TrMDHc8  : ---------------------- :   -
TrMDHc9  : ---------------------- :   -
TrMDHc10 : ---------------------- :   -
TrMDHc11 : ---------------------- :   -
TrMDHc12 : ---------------------- :   -
TrMDHc13 : ---------------------- :   -
TrMDHc14 : ---------------------- :   -
TrMDHc15 : ---------------------- :   -
TrMDHc16 : ---------------------- :   -
TrMDHc17 : TGGNCANCGATACACANCCCCC : 465
```

Figure 64 Consensus contig nucleotide sequence of TrMDHd

```
                  *        20         *        40         *        60
TrMDHd : GGGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTCAACTTCTCTTTCCATT :  60

                  *        80         *       100         *       120
TrMDHd : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 120

                  *       140         *       160         *       180
TrMDHd : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 180

                  *       200         *       220         *       240
TrMDHd : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240

                  *       260         *       280         *       300
TrMDHd : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300

                  *       320         *       340         *       360
TrMDHd : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 360

                  *       380         *       400         *       420
TrMDHd : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420

                  *       440         *       460         *       480
TrMDHd : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480

                  *       500         *       520         *       540
TrMDHd : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540

                  *       560         *       580         *
TrMDHd : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAGAAA : 598
```

Figure 65 Deduced amino acid sequence of TrMDhd

```
                     *        20         *        40         *        60
TrMDHd : MAASAAATFTIGTAQTGRPLPQSNPFGLKVNSQVNFKTFSGLKAMSSLRCESESSFFGNE :  60

                     *        80         *       100         *       120
TrMDHd : TSAALRATFAPKAQKENQNINRNLHPQASYKVAVLGAAGGIGQPLALLIKMSPLVSDLHL : 120

                     *       140         *       160
TrMDHd : YDIANVKGVAADISHCNTPSKVLDFTGASELANCLKGVDVVVIPAGVPR : 169
```

Figure 66 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHd

```
                     *        20         *        40         *        60
TrMDHd1 : GNGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTNAACTTCTCTTTCCATT :  60
TrMDHd2 : -GTTAGGCGGAGATTNNAACCCATTTTCCTCTTAAATCTCTCTC-ACTTCTCTTTCCATT :  58
TrMDHd3 : -------GGGAGATTTNAACCCATTTTCCTCTTAAATCTCTC-CGACTTCTCGTTCCATT :  52

                     *        80         *       100         *       120
TrMDHd1 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 120
TrMDHd2 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 118
TrMDHd3 : CCCATTACCATTCATTCCCAGACGTTGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 112

                     *       140         *       160         *       180
TrMDHd1 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 180
TrMDHd2 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 178
TrMDHd3 : TTGGAACTGCCCAAACAGGGAGGTCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 172

                     *       200         *       220         *       240
TrMDHd1 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240
TrMDHd2 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 238
TrMDHd3 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCGTCTCTAAGATGCG : 232

                     *       260         *       280         *       300
TrMDHd1 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300
TrMDHd2 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 298
TrMDHd3 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTTGTGCTGCTCTGCGTGCAACTTTTGCAC : 292

                     *       320         *       340         *       360
TrMDHd1 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 360
TrMDHd2 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 358
TrMDHd3 : CCAAAGCTCAAAAGGAAAACCGAAACATCAACCGCAATTTGCAGCCTCAGGCATCCTACA : 352

                     *       380         *       400         *       420
TrMDHd1 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420
TrMDHd2 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 418
TrMDHd3 : AAGTGGCGGTTCTCGGTGCTGCAGGAGGAATTGGTCAGCCACTTGCACTTCTCATTAAGA : 412

                     *       440         *       460         *       480
TrMDHd1 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480
TrMDHd2 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 478
TrMDHd3 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGACATTGCGAATGTTAAGGGAGTTGCTG : 472

                     *       500         *       520         *       540
TrMDHd1 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540
TrMDHd2 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 538
TrMDHd3 : CTGATATCAGCCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGC : 532

                     *       560         *       580         *
TrMDHd1 : TGGCAAATTGTTTG-------------------------------------------- : 554
TrMDHd2 : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAG--- : 593
TrMDHd3 : TAGCAAATTGTTTGAAAGGTGTGGATGTTGTTGTTATACCTGCTGGTGTTCCTAGAAA : 590
```

Figure 67 Consensus contig nucleotide sequence of TrMDHe

```
                 *        20         *        40         *        60
TrMDHe : TTNTNTTTATTTTATGTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTGTG :  60

                 *        80         *       100         *       120
TrMDHe : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG : 120

                 *       140         *       160         *       180
TrMDHe : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 180

                 *       200         *       220         *       240
TrMDHe : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 240

                 *       260         *       280         *       300
TrMDHe : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 300

                 *       320         *       340         *       360
TrMDHe : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 360

                 *       380         *       400         *       420
TrMDHe : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 420

                 *       440         *       460         *       480
TrMDHe : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 480

                 *       500         *       520         *       540
TrMDHe : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 540

                 *       560         *       580         *       600
TrMDHe : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 600

                 *       620         *       640         *       660
TrMDHe : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAGGGGTTACA : 660

                 *       680         *       700         *       720
TrMDHe : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA : 720

                 *       740         *       760         *       780
TrMDHe : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA : 780

                 *       800         *       820         *       840
TrMDHe : CAGGTTAAGCCTCCCAGTAGCTTCACCGCAGAAGAAACCGAATACCTGACAAANCGCATT : 840

                 *       860         *       880         *       900
TrMDHe : CAAAANGGCGGAACACAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTN : 900

                 *       920         *       940         *       960
TrMDHe : ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC : 960
```

```
                     *        980         *        1000          *        1020
TrMDHe : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC : 1020

                     *       1040         *        1060          *        1080
TrMDHe : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG : 1080

                     *       1100         *        1120          *        1140
TrMDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

                     *       1160         *        1180          *        1200
TrMDHe : GTAGAATTCATCAAAAAAAAANAAAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 1200

                     *       1220         *
TrMDHe : ATATCTATAAAGAACTTGTGTAATAATTCC : 1230
```

Figure 68 Deduced amino acid sequence of TrMDHe

```
                   *        20         *        40         *        60
TrMDHe : MEAHAAGANQRIARISAHLQPPNFQEGGDVAISKANCRAKGGAPGFKVAILGAAGGIGQS :  60

                   *        80         *       100         *       120
TrMDHe : LSLLLKINPLVSVLHLYDVVNTPGVTADVSHIDTGAVVRGFLGQAQLENALTGMDLVVIP : 120

                   *       140         *       160         *       180
TrMDHe : AGVPRKPGMTRDDLFKINAGIVRTLSEGIAKSCPNAIVNLISNPVNSTVPIAAEVFKKAG : 180

                   *       200         *       220         *       240
TrMDHe : TYDPKRLLGVTTLDVVRANTFVAEVLGVDPREVDVPVVGGHAGVTILPLLSQVKPPSSFT : 240

                   *       260         *       280         *       300
TrMDHe : AEETEYLTXRIQXGGTQVVEAKAGAGSATLMAYAAAKFANACLRGLKGEAGIVECAFVDS : 300

                   *       320         *       340         *
TrMDHe : QVTELPFFAAKVRLGRGGAEEIYQLGPLNEYERIGLEKAKKELAGSIQKGVEFIKKKXR : 359
```

Figure 69 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHe

```
                    *        20         *        40         *        60
TrMDHe1  : TTNTNTTTATTTATGTTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTCTG :  60
TrMDHe2  : ---------------------------------------------------------GNG :   3
TrMDHe3  : ---------------------------------------------------------GTG :   3
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
TrMDHe1  : TCTCT-AATTATTATTAGTCCTTCGAAATGGAAGCACATGCAGCTGGTACCAATCAGAGG : 119
TrMDHe2  : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGTGCCAATCAGAGG :  63
TrMDHe3  : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCCCATGCAGCTGGAGCCAATCAGAGG :  63
TrMDHe4  : --------------GNAGTCCTTANAAATGGAAGCACATGCAGCTGGAGCC-ATC-GAGG :  44
TrMDHe5  : ----------------------GAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG :  38
TrMDHe6  : ----------------------------------CCANTGCAGCTGGTGCCANTNNGAGG :  26
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       140         *       160         *       180
TrMDHe1  : ATTGCAAGAATCTCTGCTCATCTTCAGCCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 179
TrMDHe2  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 123
TrMDHe3  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 123
TrMDHe4  : ATTGCAAGAATCTCTGCTCATCTTC-GCCTCCAAATTTCCAGGAAGGAAGTGATGTCGCA : 103
TrMDHe5  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA :  98
TrMDHe6  : ATTGC-AGAATCTCTGCTCATCTT-NACCTCC-AATTTCCAGGAAGGAGGTGATGTTGCA :  83
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       200         *       220         *       240
TrMDHe1  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 239
TrMDHe2  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe3  : ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe4  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 163
TrMDHe5  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 158
TrMDHe6  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 143
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

```
                      *        260         *        280         *        300
TrMDHe1  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 299
TrMDHe2  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 243
TrMDHe3  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 243
TrMDHe4  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 223
TrMDHe5  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 218
TrMDHe6  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 203
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                      *        320         *        340         *        360
TrMDHe1  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 359
TrMDHe2  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 303
TrMDHe3  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 303
TrMDHe4  : TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 283
TrMDHe5  : TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 278
TrMDHe6  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 263
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                      *        380         *        400         *        420
TrMDHe1  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 419
TrMDHe2  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 363
TrMDHe3  : ATTGATACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 363
TrMDHe4  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 343
TrMDHe5  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 338
TrMDHe6  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 323
TrMDHe7  : --------------------------------------GTTTCAACTTGAAAATGCACTT :  22
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                      *        440         *        460         *        480
TrMDHe1  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 479
TrMDHe2  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 423
TrMDHe3  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 423
TrMDHe4  : ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 403
TrMDHe5  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 398
TrMDHe6  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 383
TrMDHe7  : ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG :  82
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                      *        500         *        520         *        540
TrMDHe1  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 539
TrMDHe2  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 483
TrMDHe3  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 483
TrMDHe4  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 463
TrMDHe5  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 458
TrMDHe6  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 443
TrMDHe7  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 142
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

```
                  *      560          *      580          *      600
TrMDHe1  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 599
TrMDHe2  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 543
TrMDHe3  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 543
TrMDHe4  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 523
TrMDHe5  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 518
TrMDHe6  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 503
TrMDHe7  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 202
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                  *      620          *      640          *      660
TrMDHe1  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTANGGGTAACA : 659
TrMDHe2  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACAT----------------------------- : 574
TrMDHe3  : GCTGCTGAGGTCTTCAAGAAAGCCGGTACATAT--------------------------- : 576
TrMDHe4  : GCTGCTGAGGTCTTCAAGAAAGCCGGTACATATGATCCAAAACGACTTTTAGGAGTTACA : 583
TrMDHe5  : GCTGGTGAGGTCTTCAAGAAAGCCGGNACATATGATCCAAAACNACTTTTAAGGGTTACA : 578
TrMDHe6  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAG-------- : 555
TrMDHe7  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATTCAAAGCGACTTTTAGGGGTAACA : 262
TrMDHe8  : ------------------------------TATGATCC-ACGCGACTTTTAGG-GGTACA :  28
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                  *      680          *      700          *      720
TrMDHe1  : ACCCTCGATGNTGT---------------------------------------------- : 673
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ACCCTCGATG-------------------------------------------------- : 593
TrMDHe5  : ACCCTNGATGTTGNGAGGGCAAATACTTTTGTGGCANAAG-NCTTGGNGTTGANCCCAAA : 637
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA : 322
TrMDHe8  : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA :  88
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                  *      740          *      760          *      780
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : NAGGGTNATNTTCCANTGGTAGGAGGGCGCCCNGGANT-ACAANATTACC-CTTTTTT-- : 693
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : GAGGTTGATGTTCCAGNGGTAGGATGGCACGCANGAGT-ACAATATTACCTCTTTTGTCA : 381
TrMDHe8  : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA : 148
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                  *      800          *      820          *      840
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : CAGGTTAAGCCTNCCAGTANCTT-ACCGNAGAANAAACCGAATACCTGACANANCGNATT : 440
TrMDHe8  : CAGGTTAAGCCTCCCAGTAGCTTCACTGCAGAAGAAACCGAATACCTGACAAATCGCATT : 208
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

```
                 *      860         *      880         *      900
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : CAAAANGGCGGAACACAAGTCGTTGAGGCAAAG--------------------------- :  473
TrMDHe8  : CAAAATGGTGGAACAGAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTA :  268
TrMDHe9  : ------------------GTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTN :   42
TrMDHe10 : -------------------TTGTTGAGGNAAAGGCTGGGGCTGGTTCGG-NAC-CT-NTN :   38

                 *      920         *      940         *      960
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : ATGGCATATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :  328
TrMDHe9  : ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :  102
TrMDHe10 : ATGGCCTATGCAGCTGCC-AGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :   97

                 *      980         *     1000         *     1020
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  388
TrMDHe9  : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  162
TrMDHe10 : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  157

                 *     1040         *     1060         *     1080
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATAGCAACTTGGTCCCCTTAATGAG :  448
TrMDHe9  : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG :  222
TrMDHe10 : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG :  217

                 *     1100         *     1120         *     1140
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : TATGAGAGGATTGGGTTGGAAAAAGCGAAGAATGAGTTAGCGGGAAGCATCCAGAAGGGA :  508
TrMDHe9  : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA :  282
TrMDHe10 : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA :  277
```

```
                 *        1160         *        1180         *        1200
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : GTAGAATTCATCAGAAAATAAGTCAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 568
TrMDHe9  : GTAGAATTCATCAGANAAAAANAA------------------------------------ : 306
TrMDHe10 : GTAGAATTCATCAAAAAAAAAN-------------------------------------- : 299

                 *        1220         *
TrMDHe1  : ------------------------------ :   -
TrMDHe2  : ------------------------------ :   -
TrMDHe3  : ------------------------------ :   -
TrMDHe4  : ------------------------------ :   -
TrMDHe5  : ------------------------------ :   -
TrMDHe6  : ------------------------------ :   -
TrMDHe7  : ------------------------------ :   -
TrMDHe8  : ATATCTATAAAGAACTTGTGTAATAATTCC : 598
TrMDHe9  : ------------------------------ :   -
TrMDHe10 : ------------------------------ :   -
```

Figure 70 Consensus contig nucleotide sequence of TrMDHf

```
                    *        20         *        40         *        60
TrMDHf : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60

                    *        80         *       100         *       120
TrMDHf : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

                    *       140         *       160         *       180
TrMDHf : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

                    *       200         *       220         *       240
TrMDHf : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

                    *       260         *       280         *       300
TrMDHf : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTTNAGTTCTTCATCTTTATGATG : 300

                    *       320         *       340         *       360
TrMDHf : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 360

                    *       380         *       400         *       420
TrMDHf : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420

                    *       440         *       460         *       480
TrMDHf : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

                    *       500         *       520         *       540
TrMDHf : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

                    *       560         *       580         *       600
TrMDHf : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 600

                    *       620         *       640         *       660
TrMDHf : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

                    *       680         *       700         *       720
TrMDHf : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 720

                    *       740         *       760         *       780
TrMDHf : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 780

                    *       800         *       820         *       840
TrMDHf : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 840

                    *       860
TrMDHf : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866
```

Figure 71 Deduced amino acid sequence of TrMDHf

```
                  *        20         *        40         *        60
TrMDHf : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ :  60

                  *        80         *       100         *       120
TrMDHf : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

                  *       140         *       160         *       180
TrMDHf : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

                  *       200         *       220         *       240
TrMDHf : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF : 240

                  *       260
TrMDHf : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268
```

Figure 72 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHf

```
                     *        20         *        40         *        60
TrMDHf1 : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                     *        80         *       100         *       120
TrMDHf1 : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                     *       140         *       160         *       180
TrMDHf1 : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                     *       200         *       220         *       240
TrMDHf1 : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240
TrMDHf2 : ------------------------------------------------GTGNCATAGGTN :  12
TrMDHf3 : ------------------------------------------------------------ :   -

                     *       260         *       280         *       300
TrMDHf1 : AACCTCTTTCAATGTTGATGAAGATGAATCCGTTGGTTT-AGTTCTTCATCTTTATGATG : 299
TrMDHf2 : ACCCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCTTCATCTTTATGATG :  70
TrMDHf3 : -------------------------------TTTGGTTTNNGTTCTTATNCTTTATGATG :  29

                     *       320         *       340         *       360
TrMDHf1 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCACATGGATACTGGTGCTGTTGTTC : 359
TrMDHf2 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 130
TrMDHf3 : TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTC :  86

                     *       380         *       400         *       420
TrMDHf1 : GAGGATTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 419
TrMDHf2 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 190
TrMDHf3 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 146

                     *       440         *       460         *       480
TrMDHf1 : TTCCTGCTGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 479
TrMDHf2 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 250
TrMDHf3 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 206

                     *       500         *       520         *       540
TrMDHf1 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCGAAGCGATGTCCTAAGGCGATTGTCA : 539
TrMDHf2 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 310
TrMDHf3 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGGTTGTCA : 266

                     *       560         *       580         *       600
TrMDHf1 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCC--------------------------- : 572
TrMDHf2 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 370
TrMDHf3 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 326
```

```
                    *        620         *        640         *        660
TrMDHf1 : ------------------------------------------------------------ :   -
TrMDHf2 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 430
TrMDHf3 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 386

                    *        680         *        700         *        720
TrMDHf1 : ------------------------------------------------------------ :   -
TrMDHf2 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 490
TrMDHf3 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 446

                    *        740         *        760         *        780
TrMDHf1 : ------------------------------------------------------------ :   -
TrMDHf2 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 550
TrMDHf3 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 506

                    *        800         *        820         *        840
TrMDHf1 : ------------------------------------------------------------ :   -
TrMDHf2 : TCACGACAAAGGAAATTGAGTACTTG---------------------------------- : 576
TrMDHf3 : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 566

                    *        860
TrMDHf1 : -------------------------- :   -
TrMDHf2 : -------------------------- :   -
TrMDHf3 : TTGAGGCCAAAGCTGGAGCTGGCTCT : 592
```

Figure 73 Consensus contig nucleotide sequence of TrMDHg

```
                   *        20         *        40         *        60
TrMDhg : GTAGGCAGCATCTAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAA :  60

                   *        80         *       100         *       120
TrMDhg : TACGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGT : 120

                   *       140         *       160         *       180
TrMDhg : TAGATACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGG : 180

                   *       200         *       220         *       240
TrMDhg : TGCTGCAGGACAAATTGGNTATGCTCTTGNTCCAATGATTGCAAGAGGGATGATGCTAGG : 240

                   *       260         *       280         *       300
TrMDhg : CCCAAATCAACCTGGAATTCTTCATATGCTNGATATTGAACCAGGATTAGAGGCCCTTAA : 300

                   *       320         *       340         *       360
TrMDhg : AGGGGTGAAGATGGAACTGATTGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTAC : 360

                   *       380         *       400         *       420
TrMDhg : TACGGATGTTGTTGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCC : 420

                   *       440         *       460         *       480
TrMDhg : AAGGAAGGAAGGAATGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGC : 480

                   *       500         *       520         *       540
TrMDhg : TCAAGCTTCAGCTTTGGAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAA : 540

                   *       560         *       580         *
TrMDhg : TCCAGCAAACACAAATGCTCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 599
```

Figure 74 Deduced amino acid sequence of TrMDHg

```
                         *        20         *        40         *        60
TrMDhg : MCGLLKVDKEPVTVLVTGAAGQIXYALXPMIARGMMLGPNQPGILHMXDIEPGLEALKGV :  60

                         *        80         *       100         *       120
TrMDhg : KMELIDGAFPLLRGVVATTDVVEACKDVNIAVMLGGSPRKEGMERKDVMSKNVSIYKAQA : 120

                         *       140         *
TrMDhg : SALEEHAAADCKVLVVANPANTNALILKEFAPSIPEK : 157
```

Figure 75 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHg

```
                        *        20         *        40         *        60
TrMDHg1 : GTAGGCATCA--TAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA :  60
TrMDHg2 : ----GNNGGATCTAACAG-ACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA :  57

                *        80         *       100         *       120
TrMDHg1 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 122
TrMDHg2 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 119

              *       140         *       160         *       180
TrMDHg1 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 184
TrMDHg2 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 181

            *       200         *       220         *       240
TrMDHg1 : AGGACAAATTGGNTATGCTCTTGNTNCAATGATTGCNANAGGGATGATGCTANGNCCAAATC : 246
TrMDHg2 : AGGACAAATTGGTTATGCTCTTGTTCCAATGATTGCAAGAGGGATGATGCTAGGCCCAAATC : 243

          *       260         *       280         *       300         *
TrMDHg1 : NACCTGGNATTGTTGATATGCTNGNTNTTG-------------------------------- : 276
TrMDHg2 : AACCTGTAATTCTTCATATGCTTGATATTGAACCAGGATTAGAGGCCCTTAAAGGGGTGAAG : 305

                320         *       340         *       360         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : ATGGAACTGATTGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTACTACGGATGTTGT : 367

              380         *       400         *       420         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : TGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCCAAGGAAGGAAGGAA : 429

            440         *       460         *       480         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : TGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGCTCAAGCTTCAGCTTTG : 491

          500         *       520         *       540         *       5
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : GAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAATCCAGCAAACACAAATGC : 553

          60        *       580         *
TrMDHg1 : ----------------------------------------- :   -
TrMDHg2 : TCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 594
```

Figure 76 Consensus contig nucleotide sequence of TrMDHh

```
                   *        20         *        40         *        60
TrMDHh : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60

                   *        80         *       100         *       120
TrMDHh : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

                   *       140         *       160         *       180
TrMDHh : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

                   *       200         *       220         *       240
TrMDHh : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

                   *       260         *       280         *       300
TrMDHh : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTTNAGTTCTTCATCTTTATGATG : 300

                   *       320         *       340         *       360
TrMDHh : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 360

                   *       380         *       400         *       420
TrMDHh : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420

                   *       440         *       460         *       480
TrMDHh : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

                   *       500         *       520         *       540
TrMDHh : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

                   *       560         *       580         *       600
TrMDHh : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 600

                   *       620         *       640         *       660
TrMDHh : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

                   *       680         *       700         *       720
TrMDHh : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 720

                   *       740         *       760         *       780
TrMDHh : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 780

                   *       800         *       820         *       840
TrMDHh : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 840

                   *       860
TrMDHh : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866
```

Figure 77 Deduced amino acid sequence of TrMDHh

```
                 *        20         *        40         *        60
TrMDHh : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ :  60

                 *        80         *       100         *       120
TrMDHh : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

                 *       140         *       160         *       180
TrMDHh : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

                 *       200         *       220         *       240
TrMDHh : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF : 240

                 *       260
TrMDHh : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268
```

Figure 78 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHh

```
                   *        20         *        40         *        60
TrMDHh1 : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
TrMDHh1 : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
TrMDHh1 : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
TrMDHh1 : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240
TrMDHh2 : ------------------------------------------------GTGNCATAGGTN :  12
TrMDHh3 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
TrMDHh1 : AACCTCTTTCAATGTTGATGAAGATGAATCCCTTGGTTT-AGTTCTTCATCTTTATGATG : 299
TrMDHh2 : ACCCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCTTCATCTTTATGATG :  70
TrMDHh3 : -------------------------------TTTGGTTTNNGTTCTTATNCTTTATGATG :  29

                   *       320         *       340         *       360
TrMDHh1 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCACATGGATACTGGTGCTGTTGTTC : 359
TrMDHh2 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 130
TrMDHh3 : TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTC :  86

                   *       380         *       400         *       420
TrMDHh1 : GAGGATTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 419
TrMDHh2 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 190
TrMDHh3 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 146

                   *       440         *       460         *       480
TrMDHh1 : TTCCTGCTGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 479
TrMDHh2 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 250
TrMDHh3 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 206

                   *       500         *       520         *       540
TrMDHh1 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCGAAGCGATGTCCTAAGGCGATTGTCA : 539
TrMDHh2 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 310
TrMDHh3 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGGTTGTCA : 266

                   *       560         *       580         *       600
TrMDHh1 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCC--------------------------- : 572
TrMDHh2 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 370
TrMDHh3 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 326
```

```
                  *        620         *        640         *        660
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 430
TrMDHh3 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 386

                  *        680         *        700         *        720
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 490
TrMDHh3 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 446

                  *        740         *        760         *        780
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 550
TrMDHh3 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 506

                  *        800         *        820         *        840
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : TCACGACAAAGGAAATTGAGTACTTG---------------------------------- : 576
TrMDHh3 : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 566

                  *        860
TrMDHh1 : -------------------------- :   -
TrMDHh2 : -------------------------- :   -
TrMDHh3 : TTGAGGCCAAAGCTGGAGCTGGCTCT : 592
```

Figure 79 Consensus contig nucleotide sequence of TrMDHi

```
                    *        20         *        40         *        60
TrMDHi : GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTTCCTTCCTTCTTACACCTTCTCTTA :  60

                    *        80         *       100         *       120
TrMDHi : TCAACTTTCCACCTCTGAACAAAACTTCAATCTTTTCTCATTTTCTTATACCCTTTTACA : 120

                    *       140         *       160         *       180
TrMDHi : AACTTCTTCATAAAGTGTTAGGTTTTTTTTATTACTCTTTTCAAGAACCACAAAAACAG : 180

                    *       200         *       220         *       240
TrMDHi : TGTTTCTTGAATTCTTTGGAATTTTTTTTTTCCTGCAACCATGGCCTTGGCACACTTAAA : 240

                    *       260         *       280         *       300
TrMDHi : CAACCCCACTTGCTCAAAAACTCAACTTCACTCATCACAACTCTCATTTCTCTCTAGGAC : 300

                    *       320         *       340         *       360
TrMDHi : TCTCCCTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAAT : 360

                    *       380         *       400         *       420
TrMDHi : TACTTGTTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAA : 420

                    *       440         *       460         *       480
TrMDHi : GAATAAGCCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGA : 480

                    *       500         *       520         *       540
TrMDHi : GACAAAATCCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTC : 540

                    *       560         *       580         *       600
TrMDHi : CAATCATCTACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGC : 600

                    *       620         *       640
TrMDHi : GCTGAAATTATTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 647
```

Figure 80 Deduced amino acid sequence of TrMDHi

```
                     *        20          *          40          *          60
TrMDHi : MALAHLNNPTCSKTQLHSSQLSFLSRTLPRQYHCTFAPLHRTQHGRITCSVAPNQVQAPA :  60

                     *        80          *         100          *         120
TrMDHi : VQSQDPKNKPDCYGVFCLTYDLKAEEETKSWKKLINIAVSGAAGMISNHLLFKLASGEVF : 120

                     *       140
TrMDHi : GPNQPIALKLLGSERSFQALEG : 142
```

Figure 81 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHi

```
                    *        20         *        40         *        60
TrMDHi1 : GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTTCCTTCCTTCTTACA-CTTCTCTTGT :  60
TrMDHi2 : ----------------------------------------TTCTTAGACCTTCTCTTAT :  19

                    *        80         *       100         *       120
TrMDHi1 : CAACTTTCCACCTCTGAACAAAACTTCTATCTTTTCTCATTTTCTTATACCCTTTTAGAAA : 121
TrMDHi2 : -AACTTTCNACCTCTGAACCAAA-TT-AATCTTTTCT-ATTTTCTTATACCCTTTTACAAA :  76

                    *       140         *       160         *       180
TrMDHi1 : CTTCTTCATAAAGTGTTATTT--TTTTTTATTACTCTTTTCAAGAATCACAAAAACAGTGT : 180
TrMDHi2 : CTTCTTCATAAAGTGTTGGGTTTTTTTTTATTACTCTTTTCAAGAACCACAAAAACAGTGT : 137

                    *       200         *       220         *       240
TrMDHi1 : TTCTTGAATTCTTTGTAATTTTTTTTTTCCTGCAACCATGGCCTTGGCACAGTTAAACAAT : 241
TrMDHi2 : TTCTTGAATTC-TTGGAA-TTTTTTTTTCCTGCAACCATGGCTTTGGCACACTTAAACAAC : 196

                    *       260         *       280         *       300
TrMDHi1 : CCCACTTGCTCAAAAACTCAACTTCACTCATCACAACTCTCATTTTTGTCTAGGACTCTCC : 302
TrMDHi2 : CCCACTTGCTCAAAAACTCAACTTCATTCATCACAGCTCTCATTTCTCTCTAGGACTCTCC : 257

                    *       320         *       340         *       360
TrMDHi1 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 363
TrMDHi2 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 318

                    *       380         *       400         *       420
TrMDHi1 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 424
TrMDHi2 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 379

                    *       440         *       460         *       480
TrMDHi1 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGAGACAAAAT : 485
TrMDHi2 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGAGACAAAAT : 440

                    *       500         *       520         *       540
TrMDHi1 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 546
TrMDHi2 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 501

                    *       560         *       580         *       600         *
TrMDHi1 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGTCCAAATCAACCTATTGCGCTGA----- : 602
TrMDHi2 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGCGCTGAAATTA : 562

                  620         *       640
TrMDHi1 : ------------------------------------- :   -
TrMDHi2 : TTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 599
```

Figure 82 Nucleotide sequence of TrMDHj

```
                    *        20         *        40         *        60
TrMDHj : GCAAAGCNCTCNCNGACCTGGTGTGGAGCGAGCAGCTTTGCTAGACATAAATGGGCAGAT :  60

                    *        80         *       100         *       120
TrMDHj : TTTTGCGGAGCAGGGAAAAGCTCTAAATGCAGTCGCATCTCGCAATGTCAAAGTTATAGT : 120

                    *       140         *       160         *       180
TrMDHj : TGTGGGAAACCCTTGCAATACAAATGCATTAATATGCTTGAAGAATGCTCCAAATATTCC : 180

                    *       200         *       220         *       240
TrMDHj : TGCAAAAAATTTTCATGCTTTAACCCGTTTAGATGAGAACAGAGCAAAATGTCAGCTAGC : 240

                    *       260         *       280         *       300
TrMDHj : CCTCAAGGCAGGTGTCTTCTACGATAAAGTGTCGAATATGACGATATGGGGAAACCACTC : 300

                    *       320         *       340         *       360
TrMDHj : AACTACTCAGGTCCCCGATTTCTTAAATGCCAGAATCGATGGTTTGCCTGTCAAAGAAGT : 360

                    *       380         *       400         *       420
TrMDHj : GATTAAGGATCAAAAGTGGTTAGAGGAAGAGTTCACCGAAAAAGTTCAAAAGAGAGGTGG : 420

                    *       440         *       460         *       480
TrMDHj : CGTGCTTATTCAAAAGTGGGGAAGATCGTCTGCTGCATCAACTTCTGTGTCGATAGTTGA : 480

                    *       500         *       520         *       540
TrMDHj : TGCCATACGATCTTTGATCACTCCTACTCCGGAGGGTGATTGGTTTTCTACTGGTGTGTA : 540

                    *       560
TrMDHj : TACAGCTGGAAATCCTTATGGAATAGCTG : 569
```

Figure 83 Deduced amino acid sequence of TrMDHj

```
                  *       20        *       40        *       60
TrMDHj : QSXXXPGVERAALLDINGQIFAEQGKALNAVASRNVKVIVVGNPCNTNALICLKNAPNIP :  60

                  *       80        *      100        *      120
TrMDHj : AKNFHALTRLDENRAKCQLALKAGVFYDKVSNMTIWGNHSTTQVPDFLNARIDGLPVKEV : 120

                  *      140        *      160        *      180
TrMDHj : IKDQKWLEEEFTEKVQKRGGVLIQKWGRSSAASTSVSIVDAIRSLITPTPEGDWFSTGVY : 180

TrMDHj : TAGNPYGIA : 189
```

Figure 84 Nucleotide sequence of TrMDHk

```
                       *        20         *        40         *        60
TrMDHk : GNGTAGAACCCGTGAAGCCTTTTCCCTCCGGTCTCCCCGCTTGCGCCGTCGCCGTCAATT :  60

                       *        80         *       100         *       120
TrMDHk : GCTGCTTGTGTCGTCGCCTCCAGCTCCTCCTCCTCCACTGTGCCAACCGAATTACAAACC : 120

                       *       140         *       160         *       180
TrMDHk : AAAAAAATGGCGACTTGTTTGCAAACACAACTCCTCCACACAAGACCTTTTCAGTTTCGG : 180

                       *       200         *       220         *       240
TrMDHk : TCTTCCTCGTCGACAAGACCAACTTCCCTAAGATGTTCCGCCGCCACCCCATCCACCAAA : 240

                       *       260         *       280         *       300
TrMDHk : AAATCCTACAAAATCACTCTTCTTCCGGGTGATGGCATAGGTCCTGAAGTCGTTTCCGTC : 300

                       *       320         *       340         *       360
TrMDHk : GCTAAAGACGTTCTTCTCCTCACTGGATCCATCCATGGGATTAAACTTGAGTTTCAAGAG : 360

                       *       380         *       400         *       420
TrMDHk : AAGCTTTTGGGTGGTGCTGCTCTTGATGCTACTGGAGTTCCTTTACCTGATGATACTCTT : 420

                       *       440         *       460         *       480
TrMDHk : TCTGTTGCTAAGCAATCTGATGCTGTTCTTCTTGGTGCTATTGGAGGGTATAAATGGGAT : 480

                       *       500         *       520         *       540
TrMDHk : AAAAATGAGAAACAGCTGAAGCCAGAAACTGGATTGCTTCAGCTACGAGAAGGGCTTCAA : 540

                       *
TrMDHk : GTTTTTGCTAATCTCAGA : 558
```

Figure 85   Deduced amino acid sequence of TrMDHk

```
                   *        20         *        40         *        60
TrMDHk : MATCLQTQLLHTRPFQFRSSSSTRPTSLRCSAATPSTKKSYKITLLPGDGIGPEVVSVAK :  60

                   *        80         *       100         *       120
TrMDHk : DVLLLTGSIHGIKLEFQEKLLGGAALDATGVPLPDDTLSVAKQSDAVLLGAIGGYKWDKN : 120

                   *       140
TrMDHk : EKQLKPETGLLQLREGLQVFANLR : 144
```

Figure 86 Consensus contig nucleotide sequence of TrPEPCa

```
                    *        20         *        40         *        60
TrPEPCa : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT :  60

                    *        80         *       100         *       120
TrPEPCa : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTTACAGAAGGATGCACGTCTT : 120

                    *       140         *       160         *       180
TrPEPCa : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA : 180

                    *       200         *       220         *       240
TrPEPCa : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 240

                    *       260         *       280         *       300
TrPEPCa : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 300

                    *       320         *       340         *       360
TrPEPCa : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 360

                    *       380         *       400         *       420
TrPEPCa : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 420

                    *       440         *       460         *       480
TrPEPCa : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 480

                    *       500         *       520         *       540
TrPEPCa : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 540

                    *       560         *       580         *       600
TrPEPCa : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 600

                    *       620         *       640         *       660
TrPEPCa : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 660

                    *       680         *       700         *
TrPEPCa : ATNTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 713
```

Figure 87 Deduced amino acid sequence of TrPEPCa

```
                  *        20         *        40         *        60
TrPEPCa : XTXPNAAELGSDSLGAYVISMASSASDVLAVELLQKDARLTVCGELGRACPGGTLRVVPL :  60

                  *        80         *       100         *       120
TrPEPCa : FETVQDLRGAGAVIRKLLSIDWYRQHIIKNHNGHQEVMVGYSDSGKDAGRFTAAWELYKA : 120

                  *       140         *       160         *       180
TrPEPCa : QEDVVAACNKYDTKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAE : 180

                  *       200         *       220         *
TrPEPCa : FGLPQTAVRQLEIYTTAVLLATRRPPLPPREEKWRNLMEDXSKISCQSYRSVVYENP : 237
```

Figure 88 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCa

```
                      *        20         *        40         *        60
TrPEPCa1 : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT :  60
TrPEPCa2 : ------------------------------------------------------------ :   -
TrPEPCa3 : ------------------------------------------------------------ :   -

                      *        80         *       100         *       120
TrPEPCa1 : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTT-CAGAAGGATGCACGACTT : 119
TrPEPCa2 : ---------------------------------GNACTTTTACAGAAGGATGCACGTCTT :  27
TrPEPCa3 : ----------------------------------AGCTTTTACAGANGGATGCACGTCTT :  26

                      *       140         *       160         *       180
TrPEPCa1 : GCTGGTATTGGAGAGTTGGGAAGAGCATGTCCTGGTGGAACGTTGCGGGTTGTGCCTCTA : 179
TrPEPCa2 : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA :  87
TrPEPCa3 : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA :  86

                      *       200         *       220         *       240
TrPEPCa1 : TTTGAAACTGTGAAGGACCTAAGAGGAGCTGGTTCAGTTATCGGGAAACTTTTATCGATA : 239
TrPEPCa2 : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 147
TrPEPCa3 : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 146

                      *       260         *       280         *       300
TrPEPCa1 : GAGTGGTACCGTGAACACATCATTAAGAACCAGAATGGACATCAAGAGGTTATGGTTGGA : 299
TrPEPCa2 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 207
TrPEPCa3 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 206

                      *       320         *       340         *       360
TrPEPCa1 : TATTCTGATTCGGGTAAAGATGCTGGCCGCTTGACTGCTGCTTGGGAACTTTACAAAGCT : 359
TrPEPCa2 : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 267
TrPEPCa3 : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 266

                      *       380         *       400         *       420
TrPEPCa1 : CAGGAGGATGTTGTAGCTGCTTGCAATGATTATGGTATTAAAGTTACACTGTTTCATGGC : 419
TrPEPCa2 : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 327
TrPEPCa3 : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 326

                      *       440         *       460         *       480
TrPEPCa1 : CGTGGAGGCAGTATTGGTCGAGGTGGTGGCCCTACATATCTGGCTATTCAGTCCCAACCA : 479
TrPEPCa2 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 387
TrPEPCa3 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 386

                      *       500         *       520         *       540
TrPEPCa1 : CCTGGGTCTGTGATGGGAACACTTCGGTCTACTGAGCAGGGAGAAATGGTAGAGGCCAAG : 539
TrPEPCa2 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 447
TrPEPCa3 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 446

                      *       560         *       580         *       600
TrPEPCa1 : TTTGGGTTACCACAGATAGCTGTTAGACAACTTGANN----------------------- : 576
TrPEPCa2 : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 507
TrPEPCa3 : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 506
```

```
                     *        620         *        640         *        660
TrPEPCa1 : ------------------------------------------------------------ :   -
TrPEPCa2 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 567
TrPEPCa3 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 566

                     *        680         *        700         *
TrPEPCa1 : ----------------------------------------------------- :   -
TrPEPCa2 : ATN-------------------------------------------------- : 570
TrPEPCa3 : ATTTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 619
```

Figure 89 Consensus contig nucleotide sequence of TrPEPCb

```
                      *        20         *        40         *        60
TrPEPCb : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60

                      *        80         *       100         *       120
TrPEPCb : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

                      *       140         *       160         *       180
TrPEPCb : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180

                      *       200         *       220         *       240
TrPEPCb : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

                      *       260         *       280         *       300
TrPEPCb : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300

                      *       320         *       340         *       360
TrPEPCb : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360

                      *       380         *       400         *       420
TrPEPCb : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420

                      *       440         *       460         *       480
TrPEPCb : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480

                      *       500         *       520         *       540
TrPEPCb : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540

                      *       560         *       580         *
TrPEPCb : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598
```

[redacted]gure 90 -Deduced amino acid sequence of TrPEPCb

```
                   *        20         *        40         *        60
TrPEPCb : XRDKLYRTRERSRYLLAHGYSEIPEEATFTDVDEFLEPLELCYRSLCACGDRAIADGSLL :  60

                   *        80         *       100         *       120
TrPEPCb : DFLRQVSTFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYQDWSEEKRQEWLLSELVGK : 120

                   *       140         *       160         *       180
TrPEPCb : RPLFGPDLPQTDEIREVLETFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKN : 180

                   *
TrPEPCb : PLRVVPLFEKLADLESAPA : 199
```

Figure 91 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCb

```
                    *        20         *        40         *        60
TrPEPCb1 : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60
TrPEPCb2 : GTAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60

                    *        80         *       100         *       120
TrPEPCb1 : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120
TrPEPCb2 : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

                    *       140         *       160         *       180
TrPEPCb1 : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180
TrPEPCb2 : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180

                    *       200         *       220         *       240
TrPEPCb1 : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240
TrPEPCb2 : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

                    *       260         *       280         *       300
TrPEPCb1 : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300
TrPEPCb2 : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300

                    *       320         *       340         *       360
TrPEPCb1 : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360
TrPEPCb2 : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360

                    *       380         *       400         *       420
TrPEPCb1 : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420
TrPEPCb2 : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420

                    *       440         *       460         *       480
TrPEPCb1 : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480
TrPEPCb2 : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480

                    *       500         *       520         *       540
TrPEPCb1 : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540
TrPEPCb2 : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540

                    *       560         *       580         *
TrPEPCb1 : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598
TrPEPCb2 : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGN-------------- : 584
```

Figure 92 Consensus contig nucleotide sequence of TrPEPCc

```
                      *        20         *        40         *        60
TrPEPCc : GTCACATGACAAACNATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  60

                      *        80         *       100         *       120
TrPEPCc : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 120

                      *       140         *       160         *       180
TrPEPCc : CAAACTAGATTTTCCACCTAGGTCGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 180

                      *       200         *       220         *       240
TrPEPCc : ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 240

                      *       260         *       280         *       300
TrPEPCc : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300

                      *       320         *       340         *       360
TrPEPCc : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 360

                      *       380         *       400         *       420
TrPEPCc : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420

                      *       440         *       460         *       480
TrPEPCc : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 480

                      *       500         *       520         *       540
TrPEPCc : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 540

                      *       560         *
TrPEPCc : TTCTCATATGCTTAATTTGGCAAACTTGGCAGAGN : 575
```

Figure 93 Deduced amino acid sequence of TrPEPCc

```
                        *        20         *        40         *        60
TrPEPCc : MATPRNIEKMASIDAQLRLLAPRKVSDDDKLVEYDALLLDRFLDILQDLHGEDIRQTVQD :  60

                        *        80         *       100         *
TrPEPCc : CYELSAEYEGELKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANLAE : 110
```

Figure 94 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCc

```
                     *        20         *        40         *        60
TrPEPCc1 : GTCACATGACTNACTATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  60
TrPEPCc2 : ------TGACAAACNATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  54

                     *        80         *       100         *       120
TrPEPCc1 : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 120
TrPEPCc2 : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 114

                     *       140         *       160         *       180
TrPEPCc1 : CAAACTAGATTTTCCACCTAGGTCGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 180
TrPEPCc2 : CAAACTAGATTTTCCACCTAGGTTGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 174

                     *       200         *       220         *       240
TrPEPCc1 : ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 240
TrPEPCc2 : ATATAATAATTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 234

                     *       260         *       280         *       300
TrPEPCc1 : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300
TrPEPCc2 : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 294

                     *       320         *       340         *       360
TrPEPCc1 : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 360
TrPEPCc2 : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 354

                     *       380         *       400         *       420
TrPEPCc1 : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420
TrPEPCc2 : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 414

                     *       440         *       460         *       480
TrPEPCc1 : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTATGCCGGAGAAATTGGAGGA : 480
TrPEPCc2 : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 474

                     *       500         *       520         *       540
TrPEPCc1 : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 540
TrPEPCc2 : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 534

                     *       560         *
TrPEPCc1 : TTCTCATATGCTTAATTTGGCAAACTTGGCAGAGN : 575
TrPEPCc2 : TTN-------------------------------- : 537
```

Figure 95 Nucleotide sequence of TrPEPCd

```
                  *        20         *        40         *        60
TrPEPCd : AGAAGATCTCATGTTTGAGTTGTCTATGTGGCGCTGCAACGACGAGCTCCGTGTTAGAGC :  60

                  *        80         *       100         *       120
TrPEPCd : TGAAGAGCTTCATAGATCCTCAAAGAAAGATGCAAAACATTATATTGAGTTTTGGAAACA : 120

                  *       140         *       160         *       180
TrPEPCd : GATTCCTCCAAACGAGCCATATCGTGTTATTCTTGGAGGTGTGAGGGACAAACTGTATAA : 180

                  *       200         *       220         *       240
TrPEPCd : TACACGTGAACGTGCTCGACAGTTATTAGCAAATGGAACCTCTGACATCCTTGAAGAGAC : 240

                  *       260         *       280         *       300
TrPEPCd : AACCTTCACGAATGTTGAGCAGTTTCTGGAGCCTCTTGAACTGTGTTATAGGTCACTTTG : 300

                  *       320         *       340         *       360
TrPEPCd : TGCATGTGGTGACCGATCAATAGCAGACGGAAGCCTTCTTGATTTCTTGCGACAAGTTTC : 360

                  *       380         *       400         *       420
TrPEPCd : TACATTTGGACTTTCACTTGTAAGACTCGACATCCGTCAAGAGTCAGACAGGCACACAGA : 420

                  *       440         *       460         *       480
TrPEPCd : CGTTATGGATGCAATTACAAAACACTTGGAGATTGGATCTTACCGAGAATGGTCGGAAGA : 480

                  *       500         *       520         *       540
TrPEPCd : ACGCAGGCAGGAATGGCTCTTGTCTGAGCTTAGTGGAAAACGCCCTCTCTTCGGCCATGA : 540

                  *       560         *       580         *       600
TrPEPCd : TCTTCCTAAGACAGAAGAAATTGCCGATGTTTTAGATACCTTNCACGTNATTTCANAACT : 600

                  *       620         *       640         *       660
TrPEPCd : TNCCTCANATAGCTTTGGTGCCTATATCATCTCAATGGCAACCTCCCCATCTGATGTGCT : 660

                  *       680         *       700         *       720
TrPEPCd : AGCTGTCGAGCTTTTACAACGTGAATGTCATGTGAAGCAGCCGTTAANAGTTGTTCCACT : 720

                  *       740         *       760         *       780
TrPEPCd : GTTTGAAAAGCTCGCCNGTCTTGAGTCTGCTCCTGCTGCGGNAGCGCGTTTTTTNTTAGA : 780

                  *       800         *       820         *       840
TrPEPCd : TTGGGNCANAACCGNNNTAATGGAAAGCAGAAGTTNTGATAGGTACTCANACTNGGGAAA : 840

                  *
TrPEPCd : AGATGCTGGCCGNN : 854
```

Figure 96 Deduced amino acid sequence of TrPEPCd

```
                   *        20         *        40         *        60
TrPEPCd : EDLMFELSMWRCNDELRVRAEELHRSSKKDAKHYIEFWKQIPPNEPYRVILGGVRDKLYN :  60

                   *        80         *       100         *       120
TrPEPCd : TRERARQLLANGTSDILEETTFTNVEQFLEPLELCYRSLCACGDRSIADGSLLDFLRQVS : 120

                   *       140         *       160         *       180
TrPEPCd : TFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYREWSEERRQEWLLSELSGKRPLFGHD : 180

                   *       200         *       220         *       240
TrPEPCd : LPKTEEIADVLDTXHXISXLXSXSFGAYIISMATSPSDVLAVELLQRECHVKQPLXVVPL : 240

                   *       260         *       280
TrPEPCd : FEKLAXLESAPAAXARFXLDWXXTXXMESRSXDRYSXXGKDAGX : 283
```

Figure 97 Nucleotide sequence of TrPEPCe

```
                     *        20         *        40         *        60
TrPEPCe : GTTCACTGTCTCTCTGNCCAATTTTCCTCCCTTGTCTTCTTTTTCTTCTTCTTCCTCGTA :  60

                     *        80         *       100         *       120
TrPEPCe : TCTTACTGCCTCATTACACGGGTGAGAAGGAGTGAATTGCTCCAATGGCAACAAACAAAA : 120

                     *       140         *       160         *       180
TrPEPCe : TGGAAAAAATGGCATCAATTGATGCACAGCTTAGACAATTAGTACCAGCAAAAGTTAGTG : 180

                     *       200         *       220         *       240
TrPEPCe : AAGATGATAAACTTATTGAGTATGATGCTTTGTTGTTGGATCGGTTTCTTGATATCCTTC : 240

                     *       260         *       280         *       300
TrPEPCe : AGGATTTACATGGAGAGGATCTGAAAGATTCTGTTCAAGAAGTGTATGAACTTTCTGCGG : 300

                     *       320         *       340         *       360
TrPEPCe : AGTATGAAAGAAAGCATGATCCTAAGAAACTTGAAGAGCTCGGAAATTTGATAACAAGTT : 360

                     *       380         *       400         *       420
TrPEPCe : TAGATGCAGGAGATTCAATTGTTGTTGCTAAGTCCTTTTCGCACATGCTTAACTTGGCCA : 420

                     *       440         *       460         *       480
TrPEPCe : ACTTAGCTGAAGAGGTTCAGATTGCTCATCGTCGAAGGAACAAGTTGAAGAAAGGAGATT : 480

                     *       500         *       520         *       540
TrPEPCe : TTAGGGATGAGAGCAATGCAACTACCGAATCAGACATCGAAGAAACTCTTAAGAGACTTG : 540

                     *       560         *       580         *       600
TrPEPCe : TGTTTAATATGAAGAAATCTCCTCAGGAAGTTNTTGATGCGTTGAAGAACCNNACCGTTG : 600

                     *       620         *       640         *       660
TrPEPCe : ATTTGGTTCTTACTGCTCATCCCACTCAGTCCGTTCGANGNCCNCTGCTTCCCNNNGCCT : 660

                     *       680         *
TrPEPCe : GGNACGGGNACCGCNCTGNCTATCNNACTGNNN : 693
```

Figure 98 Deduced amino acid sequence of TrPEPCe

```
                   *        20         *        40         *        60
TrPEPCe : MATNKMEKMASIDAQLRQLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDSVQEV :  60

                   *        80         *       100         *       120
TrPEPCe : YELSAEYERKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANLAEEVQIAHRRRNK : 120

                   *       140         *       160         *       180
TrPEPCe : LKKGDFRDESNATTESDIEETLKRLVFNMKKSPQEVXDALKNXTVDLVLTAHPTQSVRXX : 180

                   *
TrPEPCe : LLPXAWXGXRXXYXTX : 196
```

gure 99   Consensus contig nucleotide sequence of TrCSa

```
                         *        20         *        40         *        60
TrCSa  :  GNNNCNCNACCATTACATTAATNACACTTTCCNCTTTCGCCTTGTTCTTTCTCTTCTCAA  :   60

                         *        80         *       100         *       120
TrCSa  :  TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCGTCT  :  120

                         *       140         *       160         *       180
TrCSa  :  TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTAAATGGCGTTCTT  :  180

                         *       200         *       220         *       240
TrCSa  :  TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC  :  240

                         *       260         *       280         *       300
TrCSa  :  TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT  :  300

                         *       320         *       340         *       360
TrCSa  :  GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG  :  360

                         *       380         *       400         *       420
TrCSa  :  TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC  :  420

                         *       440         *       460         *       480
TrCSa  :  TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC  :  480

                         *       500         *       520         *       540
TrCSa  :  AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA  :  540

                         *       560         *       580         *       600
TrCSa  :  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  :  600

                         *       620         *       640         *       660
TrCSa  :  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  :  660

                         *       680         *       700         *       720
TrCSa  :  ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT  :  720

                         *       740         *       760         *       780
TrCSa  :  GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC  :  780

                         *       800         *       820         *       840
TrCSa  :  AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA  :  840

                         *       860         *       880         *       900
TrCSa  :  TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC  :  900

                         *       920         *       940         *       960
TrCSa  :  AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA  :  960
```

```
                 *        980         *        1000         *        1020
TrCSa : TATTTCTATCCATAGTGATCATGAAGGNGGCAACGTTAGTTCTCACACAGCTCACCTAGT : 1020

                 *       1040         *        1060         *        1080
TrCSa : TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG : 1080

                 *       1100         *        1120         *        1140
TrCSa : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 1140

                 *       1160         *        1180         *        1200
TrCSa : GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 1200

                 *       1220         *        1240         *        1260
TrCSa : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 1260

                 *       1280         *        1300
TrCSa : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 1307
```

Figure 100 Deduced amino acid sequence of TrCSa

```
               *        20        *        40        *        60
TrCSa : MAFFRSVSALSKLRSRVGQQPSLANSVRWLQTPSSSNTDLYSEMKELVPEYQERVKKLKK :  60

               *        80        *       100        *       120
TrCSa : DHGSVELGKITADMVLGGMRGMTALVWLGSAVDPDEGIRFRGMTIPDCQKTLPGAFPGGE : 120

               *       140        *       160        *       180
TrCSa : PLPEAILWLLLTGKVPSKEQVDSLAHELRSRAKIPEYAYKAIDALPVSAHPMTQFSTGVM : 180

               *       200        *       220        *       240
TrCSa : ALQVESEFTKAYESGIHKSRYWEPTYEDSLNLIARLPGIAAYIYRRIYKDGKIIPLDDSL : 240

               *       260        *       280        *       300
TrCSa : DYGANYAHMLGFDDPETLEFMRLYISIHSDHEGNVSSHTAHLVASSLSDPYLAFAAALNG : 300

               *       320        *       340        *       360
TrCSa : LAGPLHGLANQEVLRWIRNIVKEFGTPNISTEQLSDYIHKTLNSGQVVPGYGHGVLRNTD : 360

               *
TrCSa : PRYTCQREFALKHLPNDP : 378
```

Figure 101 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSa

```
                   *        20         *        40         *        60
TrCSa1 : GNNNCNCNACCATTACGTTAATTACATTTTCTNCTTTCGCCTTGTTCTTTCTCTTCTCAA :  60
TrCSa2 : --------------ACATTCGTNATNCTTTTCTCTTTCGCCTTGTTCTTTCTCTTCT-AA :  45
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
TrCSa1 : TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCTTCT : 120
TrCSa2 : TATAAAGACC-ATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCTTCT : 104
TrCSa3 : -----------------TACCGNAAAC--TTNCTTNC-TACTTTTNCAACCNCTNCGNCT :  40
TrCSa4 : --------------------------------------------------GTNCGCGAAA :  10
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
TrCSa1 : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTTAATGGCGTTCTT : 180
TrCSa2 : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTTAATGGCGTTCTT : 164
TrCSa3 : TCTTNCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTAAATGGCGTTCTT : 100
TrCSa4 : TNNTTCGTTTCTAC-TTT-TNACCCT-GTTGTTTNGTTGATTGATCTAAATGGCGTTCTT :  67
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
TrCSa1 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 240
TrCSa2 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 224
TrCSa3 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTCGC : 160
TrCSa4 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 127
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
TrCSa1 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 300
TrCSa2 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 284
TrCSa3 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 220
TrCSa4 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 187
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                   *       320         *       340         *       360
TrCSa1 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 360
TrCSa2 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 344
TrCSa3 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGATCATGGAAG : 280
TrCSa4 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 247
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -
```

```
                *        380          *         400          *         420
TrCSa1 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 420
TrCSa2 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 404
TrCSa3 : TGTTGAATTGGGAAAAGTCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACAGC : 340
TrCSa4 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 307
TrCSa5 : ---------GNGGAAAAATACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC :  51
TrCSa6 : --------------------------------------------GNAGAGGAATGACTGC :  16
TrCSa7 : ------------------------------------------------------------ :   -

                *        440          *         460          *         480
TrCSa1 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 480
TrCSa2 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 464
TrCSa3 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 400
TrCSa4 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCANATGAGGGAATTCGCTTTAGGGGCATGAC : 367
TrCSa5 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 111
TrCSa6 : TTTAGTGTGGCT-GGCT-NGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC :  74
TrCSa7 : ------------------------------------------------------------ :   -

                *        500          *         520          *         540
TrCSa1 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 540
TrCSa2 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 524
TrCSa3 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTNCTGGCGGGGAGNCTTTGNCCNA : 460
TrCSa4 : AATTCCTGACTGCCACAAAACACTTGCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 427
TrCSa5 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTCTTCCTGGTGGGGAGCCTTTGCCCGA : 171
TrCSa6 : AATTCCTGACTGCCAG-AAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 133
TrCSa7 : ------------------------------------------------------------ :   -

                *        560          *         580          *         600
TrCSa1 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 600
TrCSa2 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 584
TrCSa3 : GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 520
TrCSa4 : GGCTATACTGCGGNTTNTATTGACCGGNN------------------------------- : 456
TrCSa5 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 231
TrCSa6 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 193
TrCSa7 : ------------------------------------------------------------ :   -

                *        620          *         640          *         660
TrCSa1 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 660
TrCSa2 : AGCN-------------------------------------------------------- : 588
TrCSa3 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 580
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 291
TrCSa6 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 253
TrCSa7 : ------------------------------------------------------------ :   -

                *        680          *         700          *         720
TrCSa1 : ACTGCCTGTTTCTGCTCATCCAATGACACAAN---------------------------- : 692
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 640
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 351
TrCSa6 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 313
TrCSa7 : ------------------------------------------------------------ :   -
```

```
                    *       740         *       760         *       780
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : GGAGAGTGAGTTTACAAAGGCATATGAGAGTGGATACATN-------------------- : 681
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGATACATAAGTCAAGGTATTGGGAGCC : 411
TrCSa6 : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGATACATAAGTCAAGGTATTGGGAGCC : 373
TrCSa7 : ----------------------CNTCAGAGTGGGA-NCNT-AGT-AAGG-ATTGGGAGCC :  34

                    *       800         *       820         *       840
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA : 471
TrCSa6 : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA : 433
TrCSa7 : -ACTTATGAGGAT-GCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA :  92

                    *       860         *       880         *       900
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC : 531
TrCSa6 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC : 493
TrCSa7 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC : 152

                    *       920         *       940         *       960
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA : 591
TrCSa6 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA : 553
TrCSa7 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA : 212

                    *       980         *      1000         *      1020
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : TATTTCTATN-------------------------------------------------- : 601
TrCSa6 : TATTTCTATCCATAGTGATCATGAAGGN-------------------------------- : 581
TrCSa7 : TATTTCTATCCATAGTGATCATGAAGGTGGCAACGTTAGTTCTCACACAGCTCACCTAGT : 272

                    *      1040         *      1060         *      1080
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG : 332
```

```
                 *        1100         *        1120         *        1140
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 392

                 *        1160         *        1180         *        1200
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 452

                 *        1220         *        1240         *        1260
TrCSa1 : ------------------------------------------------------------ :   -
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 512

                 *        1280         *        1300
TrCSa1 : ----------------------------------------------- :   -
TrCSa2 : ----------------------------------------------- :   -
TrCSa3 : ----------------------------------------------- :   -
TrCSa4 : ----------------------------------------------- :   -
TrCSa5 : ----------------------------------------------- :   -
TrCSa6 : ----------------------------------------------- :   -
TrCSa7 : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 559
```

gure 102 Consensus contig nucleotide sequence of TrCSb

```
                 *        20         *        40         *        60
TrCSb : CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA :   60

                 *        80         *       100         *       120
TrCSb : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATTC :  120

                 *       140         *       160         *       180
TrCSb : AAGNAGAAGAAGGAAAAACAAAATCCACACAAACAAACATCTTACAACAATGTCAACGAC :  180

                 *       200         *       220         *       240
TrCSb : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT :  240

                 *       260         *       280         *       300
TrCSb : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT :  300

                 *       320         *       340         *       360
TrCSb : TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA :  360

                 *       380         *       400         *       420
TrCSb : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA :  420

                 *       440         *       460         *       480
TrCSb : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG :  480

                 *       500         *       520         *       540
TrCSb : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT :  540

                 *       560         *       580         *       600
TrCSb : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT :  600

                 *       620         *       640         *       660
TrCSb : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT :  660

                 *       680         *       700         *       720
TrCSb : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC :  720

                 *       740         *       760         *       780
TrCSb : TCAAGATGCACATCCTATGGGCGTCCTAGTGAATGCAATAAGCGCTCTGTCTGTTTTTCA :  780

                 *       800         *       820         *       840
TrCSb : TCCTGACGCAAATCCTGCTCTCAGAGGTCTTGACATCTACAACTCAAAGCAAGTGAGAGA :  840

                 *       860         *       880         *       900
TrCSb : CAAACAAATAGCACGGATTATTGGAAAGATAACAACAATTGCTGCTGCAATTAATCTTAG :  900

                 *       920         *       940         *       960
TrCSb : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACAAACTATCTTACACAGAGAACTTCCT :  960
```

```
                 *        980         *        1000         *        1020
TrCSb : ATACATGCTTGATTCTCTAGGCAATCGGTCATATAAACCCAACCCTCAGCTAACTCGTGC : 1020

                 *       1040         *        1060         *        1080
TrCSb : ACTAGACATCATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 1080

                 *       1100         *        1120         *        1140
TrCSb : ACGACACCTTGCATCAAGCGGCGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 1140

                 *       1160         *        1180         *        1200
TrCSb : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 1200

                 *       1220         *        1240
TrCSb : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 1244
```

Figure 103 Deduced amino acid sequence of TrCSb

```
                  *        20         *        40         *        60
TrCSb : MSTTTTTTDESKLHDAARNRLATLSAHLLPSSTTSAALLHPIHLSSSSGISPPSNVKGTL :  60

                  *        80         *       100         *       120
TrCSb : TVVDERTGKKYTIEVSPDGTVKANDFKKISTGKNDKGLKLYDPGYLNTAPVRSTISYIDG : 120

                  *       140         *       160         *       180
TrCSb : DEGILRYRGYPIEELAEKSTFPEVAYLILYGNLPSANQLQEWEFAISQHSALPQGVLDLI : 180

                  *       200         *       220         *       240
TrCSb : QSMPQDAHPMGVLVNAISALSVFHPDANPALRGLDIYNSKQVRDKQIARIIGKITTIAAA : 240

                  *       260         *       280         *       300
TrCSb : INLRMAGRPPVLPSNKLSYTENFLYMLDSLGNRSYKPNPQLTRALDIIFILHAEHEMNCS : 300

                  *       320         *       340         *
TrCSb : TSAVRHLASSGVDVYTAIAGGVGALYGPLHGGANEAVLKMLSEIGSVDNIPEFIEGVX : 358
```

Figure 104 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSb

```
                    *        20         *        40         *        60
TrCSb1 : CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA :  60
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
TrCSb1 : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATTC : 120
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *       140         *       160         *       180
TrCSb1 : AATTCAAAGAAGGAAAAACAAAAT-CACACAAACAAACATCTTACAACAATGTCAACGAC : 179
TrCSb2 : --GNAGNAGAAGGAAACNC-AAATCCACAAAC-AAAAC-TCTTACAACAATGTCAACCAC :  55
TrCSb3 : --GNNGNAGAAGGAAACACAAAATNCACAAACAAAAACATCTTACAACAATGTCAACCAC :  58
TrCSb4 : ----GNAAAGAGGAAAAAC-AAAT--NCACAAAC-AACATCTTAC-ACAATGTC-ACGAC :  50
TrCSb5 : -------GNAAGGAAAAAC-AAAT--NC-CAAAC-AAC-TCTTAC-ACAATGTC-ACGAC :  45
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *       200         *       220         *       240
TrCSb1 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 239
TrCSb2 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 115
TrCSb3 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 118
TrCSb4 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTAGCCACCCT : 110
TrCSb5 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 105
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *       260         *       280         *       300
TrCSb1 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 299
TrCSb2 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 175
TrCSb3 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 178
TrCSb4 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 170
TrCSb5 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 165
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *       320         *       340         *       360
TrCSb1 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 359
TrCSb2 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 235
TrCSb3 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 238
TrCSb4 : TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 230
TrCSb5 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 225
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -
```

```
                    *        380         *        400         *        420
TrCSb1 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 419
TrCSb2 : TGAACGTACCGGGAAGAAGTATAACATTGAGGTCTCACCTGATGGCACCGTTAAAGCCAA : 295
TrCSb3 : TGAACGTACCGGGAAGAAGTATAACATTGAGGTCTCACCTGATGGCACCGTTAAAGCCAA : 298
TrCSb4 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 290
TrCSb5 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 285
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *        440         *        460         *        480
TrCSb1 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGGCTCAAACTTTATGATCCTGG : 479
TrCSb2 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 355
TrCSb3 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 358
TrCSb4 : TGATTTCAAGAAGATATCGACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 350
TrCSb5 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGGCTCAAACTTTATGATCCTGG : 345
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : -------------------------------------------------A---------- :   1

                    *        500         *        520         *        540
TrCSb1 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 539
TrCSb2 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 415
TrCSb3 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 418
TrCSb4 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 410
TrCSb5 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 405
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                    *        560         *        580         *        600
TrCSb1 : CCTTAGATATAGAGGATACCCCATTGAAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 599
TrCSb2 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 475
TrCSb3 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 478
TrCSb4 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 470
TrCSb5 : CCTTAGATATAGAGGATACCCCATTGAAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 465
TrCSb6 : --------ATAGAGGCT--CCNATTGAGGAGTTGG-CGAGAAAAGCACTTTTATGGAAGT :  49
TrCSb7 : ------------------------------------------------------------ :   -

                    *        620         *        640         *        660
TrCSb1 : GGCATATCTN-------------------------------------------------- : 609
TrCSb2 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 535
TrCSb3 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 538
TrCSb4 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 530
TrCSb5 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 525
TrCSb6 : GTCCTATCT-ATAATGTATGGAAGTTTACCTACTGAAAGTAAGTTAGCTGAATGGAATTT : 108
TrCSb7 : -------------------------------------------------GAATGGGAATT :  12

                    *        680         *        700         *        720
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATN------ : 589
TrCSb3 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCNN---- : 594
TrCSb4 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTN-------------------- : 570
TrCSb5 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC : 585
TrCSb6 : CGCTATATCTCAGCATTCAGCTGTTCCAGAAGGAGTTTTGGATATCATACAATCAATGCC : 168
TrCSb7 : TGCTATATCT-AGCATT-AGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC :  70
```

```
                 *        740         *        760         *        780
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : TCAAGNN----------------------------------------------------- : 592
TrCSb6 : TCATGATGCACATCCTATGGGTGTCCTAGTGAATGCAATAAGCGCTCTTTCTGTTTTTCA : 228
TrCSb7 : TCAAGATGCACATCCTATGGGCGTGCTTGTTAATGCTGTAAGTGCTTTGTCTGTTTTTCA : 130

                 *        800         *        820         *        840
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : TCCTGACGCCAATCCTGCTCTTAGAGGTCTTGATATTTACGACTCAAAGGAAGTGAGAGA : 288
TrCSb7 : TCCTGATGCAAATCCTGCTCTCAGAGGTCTTGACATCTACAACTCAAAGCAAGTGAGAGA : 190

                 *        860         *        880         *        900
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : CAAACAAATAGCACGGATTATTGGAAAGATTATAACAATTGCTGCTGCAGTTTATCTTAG : 348
TrCSb7 : CAAACAAATAGTGCGGATTATTGGAAAGATAACAACAATTGCTGCTGCGATTAATCTTAG : 250

                 *        920         *        940         *        960
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACGAACTATCTTACACTGAGAACTTCCT : 408
TrCSb7 : ATTGGGAGGAAGGCCACCTGTTCTTCCATCCAACAAACTTTCTTACACAGAGAACTTCCT : 310

                 *        980         *       1000         *       1020
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ATACATGCTTGATTCTTTAGGCAATCGGTCATATAAACCCAACCCTCAGCTAACTCGTGC : 468
TrCSb7 : TTACATGCTTGATTCTCTTGGCAATCGGTCATATAAACCTAATCCTCGTCTAACTCGTGC : 370

                 *       1040         *       1060         *       1080
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ACTAGACATTATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 528
TrCSb7 : ACTGGACATCATCTTCATCCTTCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 430
```

```
                 *       1100         *       1120         *       1140
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : CCGACACCTTGCATCAAGCGGCGTTGATGTATATACTGCTATTGCTGGGGN--------- : 579
TrCSb7 : ACGCCACCTTGCATCAAGTGGTGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 490

                 *       1160         *       1180         *       1200
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 550

                 *       1220         *       1240
TrCSb1 : -------------------------------------------- :   -
TrCSb2 : -------------------------------------------- :   -
TrCSb3 : -------------------------------------------- :   -
TrCSb4 : -------------------------------------------- :   -
TrCSb5 : -------------------------------------------- :   -
TrCSb6 : -------------------------------------------- :   -
TrCSb7 : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 594
```